

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds  
(without alignments)  
87.287 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_8:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34231	Synthetic
2	98	100.0	18	ADO34225	Synthetic
3	98	100.0	18	ADO34228	Synthetic
4	98	100.0	18	ADO34236	Synthetic
5	98	100.0	18	ADO34233	Synthetic
6	95	96.9	18	ADO34314	Synthetic
7	94	95.9	18	ADO34354	Synthetic
8	94	95.9	18	ADO34338	Synthetic
9	94	95.9	18	ADO34352	Synthetic
10	94	95.9	18	ADO34340	Synthetic
11	94	95.9	18	ADO34339	Synthetic
12	92	93.9	18	ADO34297	Synthetic
13	92	93.9	18	ADO34244	Synthetic
14	92	93.9	18	ADO34276	Synthetic
15	90	91.8	18	ADO34227	Synthetic
16	90	91.8	18	ADO34350	Synthetic
17	89	90.8	18	ADO34322	Synthetic
18	88	89.8	18	ADO34336	Synthetic
19	88	89.8	18	ADO34335	Synthetic
20	88	89.8	18	ADO34337	Synthetic
21	88	89.8	18	ADO34241	Synthetic
22	87	88.8	18	ADO34240	Synthetic
23	86	87.8	18	ADO34284	Synthetic

24	86	87.8	18	8	ADO34305	Ado34305 Synthetic
25	85	86.7	18	8	ADO34239	Ado34239 Synthetic
26	85	86.7	18	8	ADO34344	Ado34344 Synthetic
27	85	86.7	18	8	ADO34319	Ado34319 Synthetic
28	84	85.7	18	8	ADO34245	Ado34245 Synthetic
29	84	85.7	18	8	ADO34301	Ado34301 Synthetic
30	84	85.7	18	8	ADO34343	Ado34343 Synthetic
31	84	85.7	18	8	ADO34318	Ado34318 Synthetic
32	82	83.7	18	8	ADO34302	Ado34302 Synthetic
33	82	83.7	18	8	ADO34279	Ado34279 Synthetic
34	82	83.7	18	8	ADO34303	Ado34303 Synthetic
35	82	83.7	18	8	ADO34242	Ado34242 Synthetic
36	82	83.7	18	8	ADO34300	Ado34300 Synthetic
37	82	83.7	18	8	ADO34281	Ado34281 Synthetic
38	82	83.7	18	8	ADO34317	Ado34317 Synthetic
39	81	82.7	18	8	ADO34323	Ado34323 Synthetic
40	81	82.7	18	8	ADO34280	Ado34280 Synthetic
41	80	81.6	18	8	ADO34264	Ado34264 Synthetic
42	79	80.6	18	8	ADO34320	Ado34320 Synthetic
43	78	79.6	18	2	AAI18917	AAI18917 Lecithin:
44	78	79.6	18	2	AAI19171	AAI19171 Lecithin:
45	78	79.6	18	2	AAI19425	AAI19425 Lecithin:

#### ALIGNMENTS

RESULT 1

ADO34231  
ID ADO34231 standard; peptide; 18 AA.

XX AC ADO34231;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;  
XX KW vasotrophic; antiarteriosclerotic; cerebroprotective; antianginal;  
XX KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
XX KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
XX KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 8; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
polypeptide. The invention further comprises an isolated nucleic acid  
encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
a host cell, a recombinant cell or a transgenic, non-human subject  
(including animal or plant) comprising the synthetic apolipoprotein-E  
mimicking polypeptide encoding polynucleotide; a composition comprising  
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18  
 |||||

RESULT 2  
 ADO34225  
 ID ADO34225 standard; peptide; 18 AA.  
 XX  
 AC ADO34225;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 18 /note= "C-terminal amide"  
 FT  
 XX WO2004043403-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 13-NOV-2003; 2003WO-US036268.  
 XX  
 PR 13-NOV-2002; 2002US-0425821P.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Anantharamiah GM, Garber DW, Datta G;  
 XX  
 DR WPI; 2004-411629/38.  
 XX  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 XX  
 PS Claim 4; SEQ ID NO 2; 79pp; English.  
 XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 .CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18  
 |||||

RESULT 3  
 ADO34228  
 ID ADO34228 standard; peptide; 18 AA.  
 XX  
 AC ADO34228;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004043403-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 13-NOV-2003; 2003WO-US036268.  
 XX  
 PR 13-NOV-2002; 2002US-0425821P.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Anantharamiah GM, Garber DW, Datta G;  
 XX  
 DR WPI; 2004-411629/38.  
 XX  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 XX  
 PS Claim 4; SEQ ID NO 5; 79pp; English.  
 XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject

CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 4  
 ADO34236  
 ID ADO34236 standard; peptide; 18 AA.

XX ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 5  
 ADO34233  
 ID ADO34233 standard; peptide; 18 AA.

XX ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.  
 XX  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GIRRFGLSIWRFIRAFYIG 18  
 |||||  
 Db 1 GIRRFGLSIWRFIRAFYIG 18  
 |||||  
 RESULT 6  
 ADO34314  
 ID ADO34314 standard; peptide; 18 AA.  
 XX  
 AC ADO34314;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004043403-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 13-NOV-2003; 2003WO-US036268.  
 XX  
 PR 13-NOV-2002; 2002US-0425821P.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Anantharamiah GM, Garber DW, Datta G;  
 XX  
 DR WPI; 2004-411629/38.  
 XX  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 XX  
 PS Claim 4; SEQ ID NO 91; 79pp; English.  
 XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.  
 XX  
 XX  
 SQ Sequence 18 AA;  
 Query Match 96.9%; Score 95; DB 8; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GIRRFGLSIWRFIRAFYIG 18  
 |||||  
 Db 1 GIRRFGLSIWRFIRAFYIG 18  
 |||||  
 RESULT 7  
 ADO34354  
 ID ADO34354 standard; peptide; 18 AA.  
 XX  
 AC ADO34354;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004043403-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 13-NOV-2003; 2003WO-US036268.  
 XX  
 PR 13-NOV-2002; 2002US-0425821P.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Anantharamiah GM, Garber DW, Datta G;  
 XX  
 DR WPI; 2004-411629/38.  
 XX  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 XX  
 PS Claim 4; SEQ ID NO 131; 79pp; English.  
 XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic



CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFFIRAFYQ 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFLRAFYQ 18

RESULT 8  
 ADO34338  
 ID ADO34338 standard; peptide; 18 AA.  
 XX  
 AC ADO34338;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.  
 XX WO2004043403-A2.  
 XX  
 XX 27-MAY-2004.  
 XX  
 XX 13-NOV-2003; 2003WO-US036268.  
 XX  
 XX 13-NOV-2002; 2002US-0425821P.  
 XX  
 XX (UABR-) UAB RES FOUND.  
 XX  
 XX Anantharamiah GM, Garber DW, Datta G;  
 XX  
 XX WPI; 2004-411629/38.  
 XX  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 XX comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 115; 79pp; English.  
 XX  
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 XX polypeptide. The invention further comprises an isolated nucleic acid  
 XX encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 XX a host cell, a recombinant cell or a transgenic, non-human subject  
 XX (including animal or plant) comprising the synthetic apolipoprotein-E  
 XX mimicking polypeptide encoding polynucleotide; a composition comprising  
 XX the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 XX an monoclonal antibody that specifically binds to the synthetic  
 XX apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFFIRAFYQ 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFFIRAFYQ 18

RESULT 9  
 ADO34352  
 ID ADO34352 standard; peptide; 18 AA.  
 XX  
 AC ADO34352;  
 XX

DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 129.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 XX comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 XX polypeptide. The invention further comprises an isolated nucleic acid  
 XX encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 XX a host cell, a recombinant cell or a transgenic, non-human subject  
 XX (including animal or plant) comprising the synthetic apolipoprotein-E  
 XX mimicking polypeptide encoding polynucleotide; a composition comprising  
 XX the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 XX an monoclonal antibody that specifically binds to the synthetic  
 XX apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 XX mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. NO. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFTRAFYG 18  
 |||||:||||:||||  
 Db 1 GIRRFGLSIWRFTRAFYG 18

RESULT 10  
 ADO34340  
 ID ADO34340 standard; peptide; 18 AA.

XX ADO34340;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. NO. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFTRAFYG 18  
 |||||:||||:||||  
 Db 1 GIRRFGLSIWRFTRAFYG 18

RESULT 11  
 ADO34339  
 ID ADO34339 standard; peptide; 18 AA.

XX ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is

Query Match 93.9%; Score 92; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
Matches 16: Conservative 2; Mismatches 0; Indels

Qy 1 GIRRFLGSIWRFIRAFYG 18  
|||:|||||||:||||  
Db 1 GIRKFLGSIWRFIRKAFYG 18

RESULT 13  
ADO34244  
ID ADO34244 standard: peptide; 18 AA.

AC ADO34244:

DT 12-AUG-2004 (first entry)

synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

apolipoprotein-E mimicking polypeptide; antilipemic; cardiac;  
KW  
KW  
antiartherosclerotic; cerebroprotective; antitumoral;  
KW  
KW  
serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
KW  
KW  
atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW  
KW  
low-density lipoprotein; triglyceride; very low density lipoprotein; VLDL;  
KW

OS Synthetic.

AA  
PN  
WO2004043403-A2.XX  
PD  
27-MAY-2004XX  
PE  
13-NOV-2003. 2003WO-IIS036268XX  
PB 13-NOV-2002. 2002HS-0425821P.XX  
PA (IIRB-) IIRB RES FOUND.

XX  
DT  
XX

XX  
DP WPT: 2004-411629/38

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
PT comprises an amino acid sequence.

XX  
PS  
Claim 4: SEQ ID NO 21: 79pp: English:

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYV 18  
 ||:|||||:|||||:|||||  
 Db 1 GIRRFLGAIWRFIRSFYV 18

RESULT 14  
 ADO34276

ID ADO34276 standard; peptide; 18 AA.

XX ADO34276;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX Synthetic.

OS Key Location/Qualifiers

FN Modified-site 1.18 /note= "All Lys residues are DiMethyl-Lysine"

PN WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYV 18  
 ||:|||||:|||||:|||||  
 Db 1 GIRRFLGSIWRFIRAFYV 18

RESULT 15

ID ADO34227 standard; peptide; 18 AA.

XX ADO34227;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking related R18L linear peptide.  
 DE apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

xx

SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.1e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18

|||||

Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:30  
Job time : 94.2857 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds  
(without alignments)  
121.233 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFTRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	49.0	627	2	S76462
2	45	45.9	178	2	A75578
3	44	44.9	461	1	G64537
4	44	44.9	589	2	A34341
5	44	44.9	806	2	A94060
6	44	44.9	861	2	H64102
7	43.5	44.4	1025	2	A93568
8	43	43.9	265	2	T32316
9	43	43.9	489	2	B84733
10	43	43.9	516	2	T33269
11	43	43.9	812	2	A46417
12	43	43.9	1607	2	T04583
13	42.5	43.4	407	2	T12085
14	42.5	43.4	760	2	E84953
15	42	42.9	107	2	T52113
16	42	42.9	214	2	D72540
17	42	42.9	228	2	T15530
18	42	42.9	237	2	B72692
19	42	42.9	246	2	I54412
20	42	42.9	258	2	F71707
21	42	42.9	258	2	D97700
22	42	42.9	273	1	HLHU69
23	42	42.9	365	1	HLHUA2
24	42	42.9	365	2	I38443
25	42	42.9	365	2	I61902
26	42	42.9	365	2	I37542
27	42	42.9	365	2	I84448
28	42	42.9	365	2	I61857
29	42	42.9	365	2	I38442

30	42	42.9	537	2	T04745
31	42	42.9	803	2	AD1282
32	42	42.9	803	2	AH1653
33	42	42.9	804	2	B89961
34	42	42.9	804	2	D69650
35	41.5	42.3	790	2	T50337
36	41	41.8	131	2	AG2115
37	41	41.8	265	2	C42595
38	41	41.8	279	2	E64109
39	41	41.8	359	2	T20575
40	41	41.8	364	2	AF2599
41	41	41.8	364	2	G97381
42	41	41.8	384	2	T08940
43	41	41.8	406	2	F96571
44	41	41.8	503	2	D96776
45	41	41.8	519	1	T02263

#### ALIGNMENTS

##### RESULT 1

S76462 hypothetical protein - Synchocystis sp. (strain PCC 6803)

C;Species: Synchocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S76462

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76462

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-627 <KAN>

A;Cross-references: UNIPROT:P74489; UNIPARC:UPI000000C103F; EMBL:D90915; GB:AB001339; NID:

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFTRAFVG 18

Db 597 GLEQLLQKIQWLQKFG 614

##### RESULT 2

A75578 transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: A75578

R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: A75578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-178 <WHI>

A;Cross-references: UNIPROT:Q9YR0; UNIPARC:UPI000000D3BE4; GB:AE001825; NID:

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRA0248

A;Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRFLGSIWRFIR 14  
| | | | |  
Db 23 ILRFLGSIWRLNR 35

RESULT 3  
G64537  
C;Species: Helicobacter pylori  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: G64537  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: G64537  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-461 <TOM>  
A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143  
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRFLGSIWRFIR 14  
: | | | | |  
Db 297 VRLLSFWRFVR 309

RESULT 4  
A34341  
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus  
C;Species: Alcaligenes eutrophus  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34341; A39190  
R;Peoples, O.P.; Sinskey, A.J.  
J. Biol. Chem. 264, 15298-15303, 1989  
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident  
A;Reference number: A34341; MUID:89359357; PMID:2670936  
A;Accession: A34341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-589 <PEO>  
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:  
R;Schubert, P.; Krueger, N.; Steinbuschel, A.  
J. Bacteriol. 173, 168-175, 1991  
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt  
omoter.  
A;Reference number: A39190; MUID:91100279; PMID:1987116  
A;Accession: A39190  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-219 <SCH>  
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:  
A;Note: the authors translated the codon TAC for residue 120 as Thr  
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC  
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;  
Best Local Similarity 47.6%; Pred. No. 33;  
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RFLGSIW-----RIFRPFY 17  
| | | | |

Db 100 RRFACDAWETNLPYRFAAFY 120

RESULT 5  
A84060  
leucyl-tRNA synthetase leus [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: A84060  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: A84060  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-806 <STO>  
A;Cross-references: UNIPROT:O9K788; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: leus  
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;  
Best Local Similarity 53.8%; Pred. No. 45;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFI 13  
| | | | |  
Db 622 GARRFLDRVWRL 634

RESULT 6  
H64102  
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)  
N;Alternate names: leucyl-tRNA synthetase  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: H64102  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: H64102  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-861 <TIGR>  
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:LA2023; NID:g15:  
C;Genetics:  
A;Gene: leus  
C;Superfamily: leucine-tRNA ligase  
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;  
Best Local Similarity 46.2%; Pred. No. 48;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFI 13  
| | | | |  
Db 665 GAKRFLGRVWNLV 677

RESULT 7  
AH3568  
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AH3568  
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.  
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letescac



Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AH3568  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1025 <KUR>  
A;Cross-references: UNIPROT:Q8YCO5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAL53715.1  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BMEI10473  
A;Map position: II  
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;  
Best Local Similarity 50.0%; Pred. No. 69;  
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSIMRFI---RAFY 17  
||||| | | | |  
Db 531 FLGSVWSFMTLPRSF 546

RESULT 8  
T32316  
hypothetical protein F31F4.4 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
C;Accession: T32316  
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.  
submitted to the EMBL Data Library, September 1997  
A;Description: The sequence of *C. elegans* cosmid F31F4.  
A;Reference number: Z21149  
A;Accession: T32316  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-265 <BLA>  
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AAB70384.  
A;Experimental source: strain Bristol N2; clone F31F4  
C;Genetics:  
A;Gene: CESP:F31F4.4  
A;Map position: 5  
A;Introns: 13/3; 67/2

C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;  
Best Local Similarity 53.8%; Pred. No. 22;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFYG 18  
||| | | | |  
Db 253 LASLWAFVHAPEG 265

RESULT 9  
B84733  
Probable cytochrome P450 [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84733  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: B84420; MUID:20083487; PMID:10617197  
A;Accession: B84733  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-489 <STO>  
A;Cross-references: UNIPROT:Q92V72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI  
C;Genetics:  
A;Gene: At2g32440

A;Map position: 2  
C;Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;  
Best Local Similarity 54.5%; Pred. No. 40;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16  
||| | | | |  
Db 54 IGNNWSFLRAF 64

RESULT 10  
T33269  
hypothetical protein C24B9.13 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33269  
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.  
submitted to the EMBL Data Library, May 1998  
A;Description: The sequence of *C. elegans* cosmid C24B9.  
A;Reference number: Z21310  
A;Accession: T33269  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-516 <MUR>  
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1  
A;Experimental source: strain Bristol N2; clone C24B9  
C;Genetics:  
A;Gene: CESP:C24B9.13  
A;Map position: 5  
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2.

Query Match 43.9%; Score 43; DB 2; Length 516;  
Best Local Similarity 41.2%; Pred. No. 42;  
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRFLGSIRFIRAFYG 18  
||| | | | |  
Db 252 LKFFITSLWFMHAFDG 268

RESULT 11  
A46417  
NIP1 protein - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 21-Sep-1993 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: A46417; S53979; S59302  
R;Gu, Z.; Moerschedl, R.P.; Sherman, F.; Goldfarb, D.S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992  
A;Title: NIP1, a gene required for nuclear transport in yeast.  
A;Reference number: A46417; MUID:93066237; PMID:1332047  
A;Accession: A46417  
A;Molecule type: DNA  
A;Residues: 1-812 <GUL>  
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:I02899  
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBI:P:117850)  
R;Connor, R.; Churcher, C.M.  
submitted to the EMBL Data Library, April 1995  
A;Reference number: S53969  
A;Accession: S53979  
A;Molecule type: DNA  
A;Residues: 571-582, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>  
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:Y  
R;Churcher, C.M.  
submitted to the EMBL Data Library, September 1995  
A;Reference number: S59302  
A;Accession: S59302  
A;Molecule type: DNA  
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>  
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS:Y  
A;Experimental source: strain AB972

## C;Genetics:

A;Gene: SGD:NIP1  
A;Cross-references: SGD:S0004926; MIPS:YMR309C  
A;Map position: 13R

Query Match 43.9%; Score 43; DB 2; Length 812;

Best Local Similarity 53.8%; Pred. No. 66; Mismatches 4; Indels 2; Gaps 0;

QY 1 GRRFLGSIWRFI 13

||| ||| : ||| |  
::| ||||: |

Db 361 GVXRILGSIISFV 373

## RESULT 12

T04583

TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C;Accession: T04583; T05507

R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.  
submitted to the Protein Sequence Database, March 1998

A;Reference number: Z15378

A;Accession: T04583

A;Molecule type: DNA

A;Residues: 1-1607 <BEV>

A;Cross-references: UNIPROT:O65506; UNIPARC:UPI000000AA45C; EMBL:AL022141

A;Experimental source: cultivar Columbia; BAC clone F23E13

R;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelke  
submitted to the Protein Sequence Database, April 1998

A;Reference number: Z15418

A;Accession: T05507

A;Molecule type: DNA

A;Residues: 1448-1607 <BE2>

A;Cross-references: UNIPARC:UPI000016DBPD; EMBL:AL022373

A;Experimental source: cultivar Columbia; BAC clone T19K4

C;Genetics:

A;Map position: 4

A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3

A;Note: F23E13.30; T19K4.270

Query Match 43.9%; Score 43; DB 2; Length 1607;

Best Local Similarity 72.7%; Pred. No. 1.3e+02; Mismatches 0; Indels 3; Gaps 0;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16

||| ||| ||| |

Db 1321 LGSSWRLIRGF 1331

## RESULT 13

T12085

reverse transcriptase homolog - fava bean (fragment)

C;Species: Vicia faba (fava bean)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T12085

R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.

submitted to the EMBL Data Library, September 1997

A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.

A;Reference number: Z17406

A;Accession: T12085

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-407 <KIN>

A;Cross-references: UNIPROT:O22103; UNIPARC:UPI000000AAD3D; EMBL:AB007466; NID:d1170509;

A;Experimental source: guard cell protoplasts

C;Superfamily: pol polyprotein

Query Match 43.4%; Score 42.5; DB 2; Length 407;

Best Local Similarity 57.9%; Pred. No. 40; Mismatches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

1 GRRFLGSIW--RFIRAF 16

Db 178 GRSFLGHVGYRRFIRDF 196

||| ||| : ||| |

## RESULT 14

E84953

penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002

C;Accession: E84953

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. AI  
A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: E84953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-760 <STO>

A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mrcB; BU200

C;Superfamily: penicillin-binding protein 1B

Query Match 43.4%; Score 42.5; DB 2; Length 760;

Best Local Similarity 44.4%; Pred. No. 74; Mismatches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFL-GSIWRFIRAFY 18

||| : ||| : |||

Db 32 INRFINGKWNPFPSIYG 49

## RESULT 15

T52113

probable transcription co-activator KIWI [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C;Accession: T52113

R;Cornack, R.S.; Hahlbrock, K.; Somesich, I.E.

Plant J. 14, 685-92, 1998

A;Title: Isolation of putative plant transcriptional coactivators using a modified two-h

A;Reference number: Z25848; MUID:98346011; PMID:9681033

A;Accession: T52113

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-107 <COR>

A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.J

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: KIWI

A;Map position: V

C;Function:

A;Description: probably plays a role in gene activation during pathogen defence and plant

C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match 42.9%; Score 42; DB 2; Length 107;

Best Local Similarity 50.0%; Pred. No. 13; Mismatches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17

||| : ||| |||

Db 54 VRNNGKIWDIREFY 69

Search completed: May 19, 2006, 14:39:56

Job time : 14.2857 secs



GO; GO:0015031; P:protein transport; IEA.  
GO; GO:0006508; P:proteolysis; IEA.  
InterPro; IPR003593; AAA\_ATPase.  
InterPro; IPR011527; ABC\_TM\_1.  
InterPro; IPR001140; ABC\_TM\_transpt.  
InterPro; IPR003439; ABC\_transp\_like.  
InterPro; IPR005074; Peptidase\_C39.  
InterPro; IPR010132; Type\_I\_sec\_HlyB.  
PANTHER; PTHR19242:SF74; Type\_I\_sec\_HlyB; 1.  
Pfam; PF00664; ABC\_membrane; 1.  
Pfam; PF00005; ABC\_tran; 1.  
Pfam; PF03412; Peptidase\_C39; 1.  
ProDom; PD000006; ABC\_transporter; 1.  
SMART; SM00382; AAA; 1.  
TIGRGRAMS; TIGR01846; type\_I\_sec\_HlyB; 1.  
PROSITE; PS00929; ABC\_TMIF; 1.  
PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
PROSITE; PS00990; PEPTIDASE\_C39; 1.  
SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;  
Best Local Similarity 62.5%; Pred No. 26;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRFFLGSIWRFIRAF 16  
| | | : | | : | |  
DQ 161 GFRWFLPAIWRYRRAP 176

RESULT 4  
Q44QD1\_CHLLI PRELIMINARY; PRT; 805 AA.  
AC Q44QD1;  
DT 13-SEP-2005, integrated into UniProtKB/TREMBL.  
DT 13-SEP-2005, sequence version 1.  
DT 21-FEB-2006, entry version 9.  
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.  
GN ORFNames=ClimDRAFT1980;  
OS Chlorobium limicola DSM 245.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium/Felodictyon group; Chlorobium.  
OX NCBI\_TaxID=290315;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DSM 245;  
RG US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
RA Hammon M., Israni S., Pitluck S., Richardson P.;  
RT "Sequencing of the draft genome and assembly of Chlorobium limicola  
DSM 245.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
RW [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DSM 245;  
RG US DOE Joint Genome Institute (JGI-ORNL);  
RA Larimer F., Land M.;  
RT "Annotation of the draft genome assembly of Chlorobium limicola DSM  
245.";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
-----  
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distributed under the Creative Commons Attribution-NoDerivs License  
-----  
CC EMBL; AAHJ01000009; EAM43320.1; -; Genomic\_DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.  
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.  
DR InterPro; IPR002302; Leu\_tRNAsyn\_Ia.  
DR Pfam; PF001133; tRNA-synt 1; 1.

```
DR PRINTS; PR00985; TRNASYNTHLEU.
DR TIGR00396; leuS_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 805 AA; 91997 MW; D4F3FE28F9592DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFI 13
DB 622 GISRFLGKWRV 634

RESULT 5
Q43K01_9CHLB
ID Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC Q43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC
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CC
CC EMBL; AAI01000002; EAM3595.1; -; Genomic_DNA.
CC DR GO; GO:000524; F:ATP binding; IEA.
CC DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
CC DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
CC DR InterPro; IPR002302; Leu_CRNAsyn_1a.
CC DR Pfam; PF00133; tRNA-synt_1; 1.
CC DR PRINTS; PR00985; TRNASYNTHLEU.
CC DR TIGRFAMs; TIGR00396; leuS_bact; 1.
CC Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFI 13
DB 622 GISRFLGKWRV 634

RESULT 6
Q39L57_BURS3
ID Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
AC Q39L57;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Verges L., Schmutz J., Larimer F., Land M., Kyripides N., Lykidis A.,
RA Richardson P.;
RA "Complete sequence of chromosome 1 of Burkholderia sp. 383."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; CP000151; AB06809.1; -; Genomic_DNA.
CC DR Complete proteome; Hypothetical protein.
CC Complete proteome; Hypothetical protein.
KW SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=BcenDRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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CC
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CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein  
CC (Potential).  
CC -!- SIMILARITY: Belongs to the XK family.  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC DR EMBL: AY534253; AAT071102.1; -; mRNA.  
CC DR Ensembl: ENSMUSG00000042631; Mus musculus.  
CC DR MGI: MGI:3526711; Xkr7.  
CC KW Membrane; Transmembrane.  
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CC FT  
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CC ID XKR7 RAT STANDARD; PRT; 580 AA.  
CC AC Q5GH56;  
CC DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.  
CC DT 01-MAR-2005, sequence version 1.  
CC DT 07-FEB-2006, entry version 8.  
CC DE XK-related protein 7.  
CC DE Names=Xkr7; Synonyms=Xrg7;  
CC OS Rattus norvegicus (Rat).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
CC OC Muridea; Muridae; Murinae; Rattus.  
CC OC NCBI\_TaxID=10116;  
CC RN [1]  
CC RP NUCLEOTIDE SEQUENCE [MRNA].  
CC RC STRAIN=Sprague-Dawley;  
CC RA Huang C.-H.; Chen Y.;  
CC RT "A superfamily of XK-related genes (XRG) widely expressed in  
CC RL vertebrates and invertebrates."  
CC RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
CC CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein  
CC (Potential).  
CC -!- SIMILARITY: Belongs to the XK family.  
CC -----  
CC CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC DR EMBL: AY534261; AAT07110.1; -; mRNA.  
CC KW Membrane; Transmembrane.  
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CC FT TRANSMEM 580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;  
CC SQ





RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;  
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;  
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";  
RL Plant Physiol. 131:335-344(2003).  
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AF37321; AA023063.1; -, mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0020037; F:heme binding; IEA.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0004497; F:monooxygenase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR01128; Cytochrome\_P450.  
DR InterPro; IPR02401; EP450I.  
DR PANTHER; PTHR19383; Cytochrome\_P450; 1.  
DR Pfam; PF00067; P450; 2.  
DR PRINTS; PR00463; EP450I.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN 1.  
DR Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;  
KW Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;  
Best Local Similarity 58.3%; Pred.No. 50;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FLGSIMRPIRAF 16  
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Db 54 FIGNWSFLRAF 65

Search completed: May 19, 2006, 14:38:12  
Job time : 115.429 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds  
(without alignments)  
63.384 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

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2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pbp.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	78	79.6	18	2	US-09-465-719-242
5	78	79.6	18	2	US-09-453-605-242
6	78	79.6	18	2	US-09-453-838-242
7	78	79.6	18	2	US-08-940-136-242
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13	78	79.6	18	2	US-09-453-834-242
14	78	79.6	18	2	US-10-283-599-242
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24	45	45.9	539	2	US-09-710-279-340
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27	44	44.9	22	1	US-08-132-167-50	Sequence 50, Appl
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29	44	44.9	1052	2	US-09-134-000C-6620	Sequence 6620, Ap
30	43	43.9	23	2	US-10-360-101-83	Sequence 83, Appl
31	43	43.9	413	3	US-09-609-146-27	Sequence 27, Appl
32	43	43.9	439	3	US-09-609-146-29	Sequence 29, Appl
33	43	43.9	683	2	US-09-902-340-15932	Sequence 15932, A
34	43	43.9	702	2	US-10-094-749-2262	Sequence 2262, Ap
35	43	43.9	812	2	US-09-538-092-643	Sequence 643, Appl
36	42	42.9	14	1	US-08-480-190-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1

US-08-940-095-242

Sequence 242, Application US/08940095

Patent No. 6004925

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/940,095

FILING DATE: 29-SEP-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6004925e

US-08-940-095-242

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Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

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Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

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; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
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; TOPOLOGY: linear
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; US-08-940-096-242

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Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
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; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
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; STRANDEDNESS: single
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; US-09-453-605-242

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; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
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; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

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Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GIKKFLGSIWKFIKAFVG 18

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; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-838-242

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US-09-453-838-242
Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
   ||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7
US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
   ||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
US-09-453-841-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
   ||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9
US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```

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; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453.833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; US-09-453-833-242

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```

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

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RESULT 10
US-09-453-826-242
; Sequence 242, Application US/09453826
; Patent No. 6630450
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6630450e
; US-09-453-826-242

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```

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

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RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids

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; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6716816e  
US-09-453-840-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18  
||:|||||:|:|:|  
Db 1 G1KKFLGSIWKFIKAFVG 18

## RESULT 12

US-09-865-989-242  
; Sequence 242, Application US/09865989  
; Patent No. 6734169  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; Sekul, Renate  
; Buttner, Klaus  
; Cornut, Isabelle  
; Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/865,989  
FILING DATE: 25-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/465,719  
FILING DATE: 17-DEC-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0006-999

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: No. 6734169e  
SEQUENCE DESCRIPTION: SEQ ID NO: 242:  
US-09-865-989-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18  
||:|||||:|:|:|  
Db 1 G1KKFLGSIWKFIKAFVG 18

## RESULT 13

US-09-453-834-242  
; Sequence 242, Application US/09453834  
; Patent No. 6753313  
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,834  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE: 29-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6753313e  
US-09-453-834-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18  
||:|||||:|:|:|  
Db 1 G1KKFLGSIWKFIKAFVG 18

## RESULT 14

US-10-283-599-242  
; Sequence 242, Application US/10283599  
; Patent No. 6844327  
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO  
SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR



TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,599

FILING DATE: 29-OCT-2002

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,136

FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0007-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6844327e

US-10-283-599-242

Query Match

Best Local Similarity 79.6%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFVG 18

DB 1 GIKKFLGSIWKFIRAFVG 18

RESULT 15

US-09-465-718-242

Sequence 242. Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/465,718

FILING DATE: 17-Dec-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/940,096

FILING DATE: 29-SEP-1997

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6900177e

US-09-465-718-242

Query Match

Best Local Similarity 79.6%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFVG 18

DB 1 GIKKFLGSIWKFIRAFVG 18

Search completed: May 19, 2006, 14:42:54

Job time : 24.8571 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds  
(without alignments)  
102.575 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28 84 85.7 18 4 US-10-712-447-22 Sequence 22, Appl  
29 84 85.7 18 4 US-10-712-447-78 Sequence 78, Appl  
30 84 85.7 18 4 US-10-712-447-95 Sequence 95, Appl  
31 84 85.7 18 4 US-10-712-447-120 Sequence 120, Appl  
32 82 83.7 18 4 US-10-712-447-19 Sequence 19, Appl  
33 82 83.7 18 4 US-10-712-447-56 Sequence 56, Appl  
34 82 83.7 18 4 US-10-712-447-58 Sequence 58, Appl  
35 82 83.7 18 4 US-10-712-447-77 Sequence 77, Appl  
36 82 83.7 18 4 US-10-712-447-79 Sequence 79, Appl  
37 82 83.7 18 4 US-10-712-447-80 Sequence 80, Appl  
38 82 83.7 18 4 US-10-712-447-94 Sequence 94, Appl  
39 81 82.7 18 4 US-10-712-447-57 Sequence 57, Appl  
40 81 82.7 18 4 US-10-712-447-100 Sequence 100, Appl  
41 80 81.6 18 4 US-10-712-447-41 Sequence 41, Appl  
42 79 80.6 18 4 US-10-712-447-97 Sequence 97, Appl  
43 78 79.6 18 3 US-09-865-989-242 Sequence 242, Appl  
44 78 79.6 18 3 US-09-865-989-242 Sequence 242, Appl  
45 78 79.6 18 4 US-10-099-574A-242 Sequence 242, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-712-447-2  
; Sequence 2, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712.447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: c-term amidated  
; OTHER INFORMATION: c-term amidated

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

Oy 1 GIRFLGSIWRFIRAFYG 18

Db 1 GIRFLGSIWRFIRAFYG 18

##### RESULT 2

US-10-712-447-5  
; Sequence 5, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712.447  
; CURRENT FILING DATE: 2003-11-13

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; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-91

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18
|||||
```



```

Query Match          95.9%;   Score 94;   DB 4;   Length 18;
Best Local Similarity 88.9%;   Pred. NO. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0;

QY      1 GIRRFLGSIWREIRAFYG 18
      |||||.:|||:||||
DB      1 GIRRFLGSLWREIRAFYG 18

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123JUS
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131

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Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0;

QY      1  GIRRFLGSIWRIFAYG 18
        |:|||||:|||||
Db       1  GIRRFLGSIWRIFAYG 18

RESULT 12
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLOPOROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-21

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Query Match	93.9%;	Score 92;	DB 4;	Length 18;
Best Local Similarity	88.9%;	Pred. No. 7.9e-07;		

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Query Match          93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GIKRFLGSIWRRPIAFYVG 18
      ||:|||||:|||||
Db       1 GIKRFLGSIWRRPIAFYG 18

RESULT 14
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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Tue May 23 08:38:01 2006

; OTHER INFORMATION: peptide  
US-10-712-447-74  
Query Match 93.9%; Score 92; DB 4; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.9e-07;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GIRKFLGSIWRFIRAFYG 18

RESULT 15  
US-10-712-447-4  
; Sequence 4, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712.447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: Patentin ver. 3.2  
; SEQ ID NO 4  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-4

Query Match 91.8%; Score 90; DB 4; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.6e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GIRRFLGSIWRFIRAFYG 18

Search completed: May 19, 2006, 15:27:56  
Job time : 81.2857 secs

**This Page Blank (uspto)**



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds  
(without alignments)  
17.943 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pap:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pap:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pap:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pap:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pap:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pap:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	38.3	441	6	US-10-511-937-2947
2	37	37.8	403	7	US-11-242-505A-18
3	36.5	37.2	60	1	US-09-949-925-142
4	36	36.7	74	1	US-09-949-925-111
5	36	36.7	599	7	US-11-302-678-5
6	34	34.7	313	7	US-11-242-505A-48
7	34	34.7	351	6	US-10-511-937-2540
8	34	34.7	447	6	US-10-975-692-2
9	34	34.7	522	6	US-10-505-928-543
10	33.5	34.2	244	7	US-11-169-140-109
11	33	33.7	342	7	US-11-204-427-7
12	33	33.7	393	7	US-11-304-129-40
13	33	33.7	393	7	US-11-304-129-48
14	33	33.7	463	6	US-10-505-928-545
15	33	33.7	1531	6	US-10-505-928-853
16	33	33.7	1534	6	US-10-505-928-40
17	33	33.7	2202	6	US-10-488-015-12
18	32.7	32.7	364	7	US-11-113-081A-6
19	32	32.7	388	6	US-10-196-749-336
20	32	32.7	388	7	US-11-024-544A-169
21	32	32.7	388	7	US-11-190-750-137
22	32	32.7	388	7	US-11-204-427-1
23	32	32.7	544	6	US-10-196-749-274
24	32	32.7	581	7	US-11-251-465-18
25	32	32.7	747	7	US-11-261-384-2

Sequence 6, Appli  
Sequence 48, Appli  
Sequence 21, Appli  
Sequence 135, Appl  
Sequence 87, Appli  
Sequence 23, Appli  
Sequence 26, Appli  
Sequence 163, Appl  
Sequence 19, Appli  
Sequence 2401, Ap  
Sequence 16, Appli  
Sequence 16, Appli  
Sequence 2, Appli  
Sequence 443, Appl  
Sequence 62, Appl  
Sequence 44, Appli  
Sequence 19, Appli  
Sequence 46, Appli  
Sequence 72, Appli  
Sequence 23, Appli

26 32 32.7 764 7 US-11-223-738-6  
27 32 32.7 1503 7 US-11-312-958-48  
28 31.5 32.1 503 7 US-11-024-544A-21  
29 31.5 32.1 503 7 US-11-190-750-135  
30 31.5 32.1 503 7 US-11-264-784-87  
31 31 31.6 126 7 US-11-075-891-23  
32 31 31.6 258 6 US-10-541-993-26  
33 31 31.6 561 6 US-10-505-928-163  
34 31 31.6 643 6 US-10-504-120-19  
35 31 31.6 651 6 US-10-511-937-2401  
36 31 31.6 667 7 US-11-311-555-16  
37 31 31.6 667 7 US-11-311-561-16  
38 31 31.6 714 6 US-10-868-498-2  
39 31 31.6 749 6 US-10-505-928-443  
40 31 31.6 919 7 US-11-302-678-62  
41 30.5 31.1 222 7 US-11-257-062-44  
42 30 30.6 269 6 US-10-511-455-19  
43 30 30.6 282 7 US-11-251-466-46  
44 30 30.6 282 7 US-11-264-784-72  
45 30 30.6 308 6 US-10-511-455-23

#### ALIGNMENTS

RESULT 1  
US-10-511-937-2947  
; Sequence 2947, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2947  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2947

Query Match 38.3%; Score 37.5; DB 6; Length 441;  
Best Local Similarity 33.3%; Pred. No. 15;  
Matches 7; Conservative 5; Mismatches 6; Indels 3; Gaps 1;

Qv 1 GIRFLGSIW---RFIRAFYG 18  
|:|||||:|  
Db 106 GLSKFLGTHLMGNILRLFG 126

RESULT 2  
US-11-242-505A-18  
; Sequence 18, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen

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; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-286P1RCP10NMIM
; CURRENT APPLICATION NUMBER: US/11/242.505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/330,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-242-505A-18

* Query Match 37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRFLGSIW 10
Db 155 VRRVLGAV 163

RESULT 3
US-09-949-925-142
; Sequence 142, Application US/09949925
; Publication No. US2006009575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match 36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRFLGSIWRF 12
Db 59 LREVSQIWRP 69

RESULT 5
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Venkateswarlu, Karicheti
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM_OMNI
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Query Match 37.2%; Score 36.5; DB 1; Length 60;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 FLGSIWRFIAPFYG 18
Db 31 FLILWIFV-APFYG 43

RESULT 4
US-09-949-925-111
; Sequence 111, Application US/09949925
; Publication No. US2006009575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match 36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRFLGSIWRF 12
Db 59 LREVSQIWRP 69

RESULT 5
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Venkateswarlu, Karicheti
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM_OMNI
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; CURRENT APPLICATION NUMBER: US/11/302,678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-302-678-5

Query Match 36.7%; Score 36; DB 7; Length 599;  
Best Local Similarity 71.4%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 LGSIWRF 12  
||:||||  
Db 64 LGNVWF 70

RESULT 6  
US-11-242-505A-48  
; Sequence 48, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
; FILE REFERENCE: MPI2001-288PRCPIONIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;  
Best Local Similarity 50.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17

Db 195 LEEAWSFLDAFY 206  
| | | | |

RESULT 7  
US-10-511-937-2540  
; Sequence 2540, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2540  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2540

Query Match 34.7%; Score 34; DB 6; Length 351;  
Best Local Similarity 46.2%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 18  
||:||||  
Db 263 LGTVLWKLMLFY 275

RESULT 8  
US-10-975-692-2  
; Sequence 2, Application US/10975692  
; Publication No. US20060090221A1  
; GENERAL INFORMATION:  
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION  
; APPLICANT: Browne, John A.  
; APPLICANT: Wallis, James G.  
; APPLICANT: Watts, Jennifer L.  
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS  
; FILE REFERENCE: 4630-58963-02  
; CURRENT APPLICATION NUMBER: US/10/975,692  
; CURRENT FILING DATE: 2004-10-26  
; PRIOR APPLICATION NUMBER: US 03/857,583  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/28655  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/111,301  
; PRIOR FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;  
Best Local Similarity 43.8%; Pred. No. 59;  
Matches 7; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 IRRLFLGSIWRFIRAFY 17  
||| : : : : :  
Db 130 IRKILETIFILFAFY 145

RESULT 9  
US-10-505-928-543  
; Sequence 543, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 543  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;  
Best Local Similarity 47.1%; Pred. No. 70;  
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 3 RRFL--GSIWRFIRAFY 17  
||| : : : : :  
Db 473 RRFTQSGDLVHRKPH 489

RESULT 10  
US-11-169-140-109  
; Sequence 109, Application US/11169140  
; Publication No. US20060099150A1  
; GENERAL INFORMATION:  
; APPLICANT: ARIZKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou, L.  
; APPLICANT: SHERIDAN, Philip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven  
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE  
; TITLE OF INVENTION: BARRIERS  
; FILE REFERENCE: 11474-037-999  
; CURRENT APPLICATION NUMBER: US/11/169,140  
; CURRENT FILING DATE: 2005-06-27  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/949,039  
; PRIOR FILING DATE: 2001-09-06  
; PRIOR APPLICATION NUMBER: 09/969,748  
; PRIOR FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 109  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Simian  
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;  
Best Local Similarity 42.1%; Pred. No. 35;  
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 GIRRLGSIW----RPIR 14  
| : : : : :  
Db 158 GLVLGAVCVARARFIR 176

RESULT 11  
US-11-204-427-7  
; Sequence 7, Application US/11204427  
; Publication No. US20060100146A1  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L  
; APPLICANT: Turkish, Aaron R  
; APPLICANT: Billheimer, Jeffrey T  
; APPLICANT: Cromley, Debra  
; TITLE OF INVENTION: AMAT-RELATED METHODS AND ARTICLES  
; FILE REFERENCE: 0575/72796/JPM/AJM/JCS  
; CURRENT APPLICATION NUMBER: US/11/204,427  
; CURRENT FILING DATE: 2005-08-15  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17  
: ||| : : : :  
Db 84 AIWRQLRDYY 93

RESULT 12  
US-11-304-129-40  
; Sequence 40, Application US/11304129  
; Publication No. US20060088915A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: TAKATSU, Yoshihiro  
; APPLICANT: WATANABE, Takuya  
; APPLICANT: TERAQ, Yasuko  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: HINUMA, Syuji  
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
; FILE REFERENCE: 2762US0P  
; CURRENT APPLICATION NUMBER: US/11/304,129  
; CURRENT FILING DATE: 2005-12-15  
; PRIOR APPLICATION NUMBER: US/10/333,192  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: JP 2000-217442  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: JP 2001-26779  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 40  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Rat  
US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;  
Best Local Similarity 46.2%; Pred. No. 75;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRPIAFY 17

Db 216 FCGIWPVDQOFY 228

## RESULT 13

US-11-304-129-48

; Sequence 48, Application US/11304129

; Publication No. US2006008915A1

; GENERAL INFORMATION:

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: MASUDA, Yasushi

; APPLICANT: TAKATSU, Yoshihiro

; APPLICANT: WATANABE, Takuya

; APPLICANT: TERAO, Yasuko

; APPLICANT: SHINTANI, Yasushi

; APPLICANT: HINUMA, Syuji

; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof

; FILE REFERENCE: 2762USOP

; CURRENT APPLICATION NUMBER: US/11/304,129

; CURRENT FILING DATE: 2005-12-15

; PRIOR APPLICATION NUMBER: US/10/333,192

; PRIOR FILING DATE: 2003-09-29

; PRIOR APPLICATION NUMBER: JP 2000-217442

; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: JP 2001-26779

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/JP01/06162

; PRIOR FILING DATE: 2001-07-17

; NUMBER OF SEQ ID NOS: 58

; SEQ ID NO 48

; LENGTH: 393

; TYPE: PRT

; ORGANISM: Mouse

US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;

Best Local Similarity 46.2%; Pred. No. 75;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRPIAFY 17

Db 216 FCGIWPVDQOFY 228

## RESULT 14

US-10-505-928-545

; Sequence 545, Application US/10505928

; Publication No. US20060089532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 545

; LENGTH: 463

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;

Best Local Similarity 33.3%; Pred. No. 90;

Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 RFLGSIWRPIAFY 18

| : : : |||

Db 339 RYYSSEYHYVGGFYG 353

## RESULT 15

US-10-505-928-853

; Sequence 853, Application US/10505928

; Publication No. US20060089532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 853

; LENGTH: 1531

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;

Best Local Similarity 50.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17

| : : : |||

Db 1122 LGLIYFFVQRFY 1133

Search completed: May 19, 2006, 15:28:17

Job time : 2.14286 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds  
(without alignments)  
87.287 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_8:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	98	100.0	18	8	ADO34231	Synthetic
2	98	100.0	18	8	ADO34225	Synthetic
3	98	100.0	18	8	ADO34228	Synthetic
4	98	100.0	18	8	ADO34236	Synthetic
5	98	100.0	18	8	ADO34233	Synthetic
6	95	96.9	18	8	ADO34314	Synthetic
7	94	95.9	18	8	ADO34354	Synthetic
8	94	95.9	18	8	ADO34338	Synthetic
9	94	95.9	18	8	ADO34352	Synthetic
10	94	95.9	18	8	ADO34340	Synthetic
11	94	95.9	18	8	ADO34339	Synthetic
12	92	93.9	18	8	ADO34297	Synthetic
13	92	93.9	18	8	ADO34244	Synthetic
14	92	93.9	18	8	ADO34276	Synthetic
15	90	91.8	18	8	ADO34227	Synthetic
16	90	91.8	18	8	ADO34350	Synthetic
17	89	90.8	18	8	ADO34322	Synthetic
18	88	89.8	18	8	ADO34336	Synthetic
19	88	89.8	18	8	ADO34335	Synthetic
20	88	89.8	18	8	ADO34337	Synthetic
21	88	89.8	18	8	ADO34241	Synthetic
22	87	88.8	18	8	ADO34240	Synthetic
23	86	87.8	18	8	ADO34284	Synthetic

24	86	87.8	18	8	ADO34305	Synthetic
25	85	86.7	18	8	ADO34239	Synthetic
26	85	86.7	18	8	ADO34344	Synthetic
27	85	86.7	18	8	ADO34319	Synthetic
28	84	85.7	18	8	ADO34245	Synthetic
29	84	85.7	18	8	ADO34301	Synthetic
30	84	85.7	18	8	ADO34343	Synthetic
31	84	85.7	18	8	ADO34318	Synthetic
32	82	83.7	18	8	ADO34302	Synthetic
33	82	83.7	18	8	ADO34279	Synthetic
34	82	83.7	18	8	ADO34303	Synthetic
35	82	83.7	18	8	ADO34242	Synthetic
36	82	83.7	18	8	ADO34300	Synthetic
37	82	83.7	18	8	ADO34281	Synthetic
38	82	83.7	18	8	ADO34317	Synthetic
39	81	82.7	18	8	ADO34323	Synthetic
40	81	82.7	18	8	ADO34280	Synthetic
41	80	81.6	18	8	ADO34264	Synthetic
42	79	80.6	18	8	ADO34320	Synthetic
43	78	79.6	18	2	AAI18917	Lecithin:
44	78	79.6	18	2	AAI19171	Lecithin:
45	78	79.6	18	2	AAI19425	Lecithin:

ALIGNMENTS

RESULT 1

ID ADO34231 standard; peptide; 18 AA.

XX ADO34231;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 8.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiac;  
KW vasotropic; antiarteriosclerotic; cerebroprotective; antidiabetic;  
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
polypeptide. The invention further comprises an isolated nucleic acid  
encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
a host cell, a recombinant cell or a transgenic, non-human subject  
(including animal or plant) comprising the synthetic apolipoprotein-E  
mimicking polypeptide encoding polynucleotide; a composition comprising  
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianigmal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
 CC Query Match 100.0%; Score 98; DB 8; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 Db 1 GIRRFLGSIWRFIRAFYG 18  
 |||||

RESULT 2  
 ADO34225  
 ID ADO34225 standard; peptide; 18 AA.  
 AC ADO34225;  
 XX 12-AUG-2004 (first entry)  
 DT Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.  
 DE  
 XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianigmal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 18 /note= "C-terminal amide"  
 FT  
 XX WO2004043403-A2.  
 PN  
 XX 27-MAY-2004.  
 PD  
 XX 13-NOV-2003; 2003WO-US036268.  
 PF  
 XX 13-NOV-2002; 2002US-0425821P.  
 PR  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Anantharamiah GM, Garber DW, Datta G;  
 PI WPI; 2004-411629/38.  
 DR  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 PS  
 XX Claim 4; SEQ ID NO 2; 79pp; English.  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianigmal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
 CC Query Match 100.0%; Score 98; DB 8; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 Db 1 GIRRFLGSIWRFIRAFYG 18  
 |||||

RESULT 3  
 ADO34228  
 ID ADO34228 standard; peptide; 18 AA.  
 AC ADO34228;  
 XX 12-AUG-2004 (first entry)  
 DT Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.  
 DE  
 XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianigmal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX Synthetic.  
 OS  
 XX WO2004043403-A2.  
 PN  
 XX 27-MAY-2004.  
 PD  
 XX 13-NOV-2003; 2003WO-US036268.  
 PF  
 XX 13-NOV-2002; 2002US-0425821P.  
 PR  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Anantharamiah GM, Garber DW, Datta G;  
 PI WPI; 2004-411629/38.  
 DR  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 PS  
 XX Claim 4; SEQ ID NO 5; 79pp; English.  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,



CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 4  
 ADO34236  
 ID ADO34236 standard; peptide; 18 AA.

AC ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 5  
 ADO34233  
 ID ADO34233 standard; peptide; 18 AA.

AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. NO. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 6

ADO34314  
 ID ADO34314 standard; peptide; 18 AA.

XX AC ADO34314;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 91; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;  
 Best Local Similarity 94.4%; Pred. NO. 1.8e-07;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 7

ADO34354

ID ADO34354 standard; peptide; 18 AA.

XX AC ADO34354;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 131; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8

ADO34338  
 ID ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9

ADO34352  
 ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 |||||:||||:|||||  
 Db 1 GIRRFLGLWRFLEAFYG 18

# RESULT 10

ADO34340  
 ID ADO34340 standard; peptide; 18 AA.

XX AC ADO34340;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 117; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 |||||:||||:|||||  
 Db 1 GIRRFIGSIWRFLEAFYG 18

# RESULT 11

ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX AC ADO34339;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 116; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.6e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18

Db 1 GLRRFGSIWRFIRAFYG 18

RESULT 12

ADO34297

ID ADO34297 standard; peptide; 18 AA.

XX

AC ADO34297;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

OS

XX WO2004043403-A2.

PN

XX 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

PI WPI; 2004-411629/38.

DR

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 74; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;

Best Local Similarity 88.9%; Pred. No. 5.3e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18

Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 13

ADO34244

ID ADO34244 standard; peptide; 18 AA.

XX

AC ADO34244;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

OS

XX WO2004043403-A2.

PN

XX 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

PI WPI; 2004-411629/38.

DR

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 21; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
SQ

Query Match 93.9%; Score 92; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYVG 18  
|||:|||||:|||||:|||||  
Db 1 GIRRFLGAIWRFIRSFYVG 18

RESULT 14  
ADO34276  
ID ADO34276 standard; peptide; 18 AA.  
AC ADO34276;  
XX  
XX  
DT 12-AUG-2004 (first entry)  
XX  
XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.  
XX  
XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
XX  
XX Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1..18  
FT /note= "All Lys residues are DiMethyl-Lysine"  
XX  
XX WO2004043403-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 13-NOV-2003; 2003WO-US036268.  
XX  
XX 13-NOV-2002; 2002US-0425821P.  
XX  
XX (UABR-) UAB RES FOUND.  
XX  
XX Anantharamiah GM, Garber DW, Datta G;  
PI WPI; 2004-411629/38.  
XX  
XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
PT comprises an amino acid sequence.  
XX  
XX Claim 4; SEQ ID NO 53; 79pp; English.  
XX  
XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
CC polypeptide. The invention further comprises an isolated nucleic acid  
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
CC a host cell, a recombinant cell or a transgenic, non-human subject  
CC (including animal or plant) comprising the synthetic apolipoprotein-E  
CC mimicking polypeptide encoding polynucleotide; a composition comprising  
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
CC an monoclonal antibody that specifically binds to the synthetic  
CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
CC mimicking polypeptide has the following activities: antilipaeamic,  
CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
SQ

Query Match 93.9%; Score 92; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYVG 18  
|||:|||||:|||||:|||||  
Db 1 GIRRFLGSIWRFIRAFYVG 18

RESULT 15  
ADO34227  
ID ADO34227 standard; peptide; 18 AA.  
XX  
XX ADO34227;  
AC  
XX  
XX 12-AUG-2004 (first entry)  
DT  
XX  
XX Synthetic apolipoprotein-E mimicking related R18L linear peptide.  
DE  
XX  
XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
XX  
XX Synthetic.  
XX  
XX  
XX WO2004043403-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 13-NOV-2003; 2003WO-US036268.  
XX  
XX 13-NOV-2002; 2002US-0425821P.  
XX  
XX (UABR-) UAB RES FOUND.  
XX  
XX Anantharamiah GM, Garber DW, Datta G;  
PI WPI; 2004-411629/38.  
XX  
XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
PT comprises an amino acid sequence.  
XX  
XX Claim 4; SEQ ID NO 4; 79pp; English.  
XX  
XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
CC polypeptide. The invention further comprises an isolated nucleic acid  
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
CC a host cell, a recombinant cell or a transgenic, non-human subject  
CC (including animal or plant) comprising the synthetic apolipoprotein-E  
CC mimicking polypeptide encoding polynucleotide; a composition comprising  
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
CC an monoclonal antibody that specifically binds to the synthetic  
CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
CC mimicking polypeptide has the following activities: antilipaeamic,  
CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX  
SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.1e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18  
| | | | | | | | | | | | | | | |  
Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:31  
Job time : 94.2857 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds  
(without alignments)  
121.233 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: Pirl1.\*

2: Pirl2.\*

3: Pirl3.\*

4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	2 S76462	hypothetical prote
2	45	45.9	178	2 A75578	transcription regu
3	44	44.9	461	1 G64537	2-oxoglutarate/mal
4	44	44.9	589	2 A34341	poly(3-hydroxybuty
5	44	44.9	806	2 A84060	leucyl-tRNA synth
6	44	44.9	861	2 A84060	leucine-tRNA ligas
7	43.5	44.4	1025	2 H43568	acridine resista
8	43	43.9	265	2 T32316	hypothetical prote
9	43	43.9	489	2 B84733	probable cytochrom
10	43	43.9	516	2 T33269	hypothetical prote
11	43	43.9	812	2 A46417	NIP1 protein - yea
12	43	43.9	1607	2 T04583	reverse transcript
13	42.5	43.4	407	2 T12085	penicillin-binding
14	42.5	43.4	760	2 E84953	probable transcrip
15	42	42.9	107	2 T52113	hypothetical prote
16	42	42.9	214	2 D72540	hypothetical prote
17	42	42.9	228	2 T15530	hypothetical prote
18	42	42.9	237	2 B72692	hypothetical prote
19	42	42.9	246	2 I54412	MHC HLA-A cell sur
20	42	42.9	258	2 F71707	o-antigen export s
21	42	42.9	258	2 D97700	o-antigen export s
22	42	42.9	273	1 HLH069	MHC class I histoc
23	42	42.9	365	1 HLH069	MHC class I histoc
24	42	42.9	365	2 I38443	gene HLA-A-0203 pr
25	42	42.9	365	2 I61902	MHC class I histoc
26	42	42.9	365	2 I37542	MHC class I histoc
27	42	42.9	365	2 I84448	MHC class I histoc
28	42	42.9	365	2 I61857	MHC HLA-A2.4a chai
29	42	42.9	365	2 I38442	gene HLA-A-0205 pr

30	42	42.9	537	2 T04745	hypothetical prote
31	42	42.9	803	2 AD1282	leucyl-tRNA synth
32	42	42.9	803	2 AH1653	leucyl-tRNA synth
33	42	42.9	804	2 B89961	leucyl-tRNA synth
34	42	42.9	804	2 D69650	leucine-tRNA ligas
35	41.5	42.3	790	2 T50337	homolog to drosoph
36	41	41.8	131	2 AG2115	hypothetical prote
37	41	41.8	265	2 C42595	rfap protein - Esc
38	41	41.8	279	2 E64109	dimethylsulfoxide
39	41	41.8	359	2 T20575	hypothetical prote
40	41	41.8	364	2 AF2599	hypothetical prote
41	41	41.8	364	2 G97381	probable permease
42	41	41.8	384	2 T08940	hypothetical prote
43	41	41.8	406	2 F96571	hypothetical prote
44	41	41.8	503	2 D96776	hypothetical prote
45	41	41.8	519	1 T02263	cytochrome P450 DW

ALIGNMENTS

RESULT 1

S76462

hypothetical protein - Synecchocystis sp. (strain PCC 6803)

C:Species: Synecchocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis

s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID:

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18

Db 597 GLEQLLKKIWQLRQKFG 614

RESULT 2

A75578

transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: A75578

R:White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75578

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <WHI>

A:Cross-references: UNIPROT:Q9RYR0; UNIPARC:UPI00000D3BE4; GB:AE001863; NID:

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0248

A:Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2; Mismatches 0; Conservative 9; Gaps 0;

QY 2 IRFLGSIWRFIR 14  
| | | | |  
Db 23 ILRFLGGIWRNLNR 35

RESULT 3  
G64537  
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: G64537  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:9739467; PMID:9252185  
A;Accession: G64537  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-461 <TOM>  
A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143  
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;  
Best Local Similarity 53.8%; Pred. No. 26; Mismatches 2; Conservative 7; Gaps 0;

QY 2 IRFLGSIWRFIR 14  
: | | | | |  
Db 297 VRLLSFWFVR 309

RESULT 4  
A34341  
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus  
C;Species: Alcaligenes eutrophus  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34341; A39190  
R;Peoples, O.P.; Sinskey, A.J.  
J. Biol. Chem. 264, 15298-15303, 1989  
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident  
A;Reference number: A34341; MUID:89359357; PMID:2670936  
A;Accession: A34341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-589 <PEO>  
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:  
R;Schubert, P.; Krueger, N.; Steinbuechel, A.  
J. Bacteriol. 173, 168-175, 1991  
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt  
omoter.  
A;Reference number: A39190; MUID:91100279; PMID:1987116  
A;Accession: A39190  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-219 <SCH>  
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:  
A;Note: the authors translated the codon TAC for residue 120 as Thr  
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc  
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;  
Best Local Similarity 47.6%; Pred. No. 33; Mismatches 5; Indels 6; Gaps 1;  
Matches 10; Conservative 0

QY 3 RRFLGSIW-----RFRAPY 17  
| | | | |

Db 100 RRPAGDAWRTNLPRFAAFY 120

RESULT 5  
A84060  
leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: A84060  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: A84060  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-806 <STO>  
A;Cross-references: UNIPROT:Q9K758; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: leuS  
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;  
Best Local Similarity 53.8%; Pred. No. 45; Mismatches 2; Conservative 7; Gaps 0;

QY 1 GIRRFLGSIWRFI 13  
| | | | |  
Db 622 GARRFLDRVWRL 634

RESULT 6  
H64102  
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)  
N;Alternate names: leucyl-tRNA synthetase  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: H64102  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, L.  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: H64102  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-861 <TIG>  
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:g15;  
C;Genetics:  
A;Gene: leuS  
C;Superfamily: leucine-tRNA ligase  
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;  
Best Local Similarity 46.2%; Pred. No. 48; Mismatches 3; Conservative 6; Indels 4; Gaps 0;

QY 1 GIRRFLGSIWRFI 13  
| | | | |  
Db 665 GAKRFLGRVWNLV 677

RESULT 7  
AH3568  
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AH3568  
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.  
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AH3568  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1025 <KUR>  
A;Cross-references: UNIPROT:Q8YCO5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAJ53715.1  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BMH10473  
A;Map position: II  
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;  
Best Local Similarity 50.0%; Pred. No. 69;  
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSIMRFI---RAFY 17  
|||||:|:|:|  
Db 531 FLGSVWSFMTLP RSFF 546

RESULT 8  
T32316  
hypothetical protein F31F4.4 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Dec-2004  
C;Accession: T32316  
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.  
A;Description: The sequence of *C. elegans* cosmid F31F4.  
A;Reference number: Z21149  
A;Accession: T32316  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-265 <BLA>  
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AA870384.  
A;Experimental source: strain Bristol N2; clone F31F4  
C;Genetics:  
A;Gene: CESP:F31F4.4  
A;Map position: 5  
A;Introns: 13/3; 67/2  
C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;  
Best Local Similarity 53.8%; Pred. No. 22;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSIMRFIRAFY 18  
|||:|:|:|  
Db 253 LASLWAFVHAFEG 265

RESULT 9  
B84733  
Probable cytochrome P450 [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84733  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: B84420; MUID:20083487; PMID:10617197  
A;Accession: B84733  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-489 <STO>  
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI  
C;Genetics:  
A;Gene: At2g32440

A;Map position: 2  
C;Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;  
Best Local Similarity 54.5%; Pred. No. 40;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIMRFIRAF 16  
|||:|:|:|  
Db 54 IGNNWSFLRAF 64

RESULT 10  
T33269  
hypothetical protein C24B9.13 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33269  
R;Murray, J.; Wohlmann, P.; Langston, Y.; O'Neal, D.  
A;Description: The sequence of *C. elegans* cosmid C24B9.  
A;Reference number: Z21310  
A;Accession: T33269  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-516 <MUR>  
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1  
A;Experimental source: strain Bristol N2; clone C24B9  
C;Genetics:  
A;Gene: CESP:C24B9.13  
A;Map position: 5  
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;  
Best Local Similarity 41.2%; Pred. No. 42;  
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 18  
|||:|:|:|  
Db 252 LKPFITSLMFMHAFDG 268

RESULT 11  
A46417  
NIP1 protein - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 21-Sep-1993 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: A46417; S53979; S59302  
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992  
A;Title: NIP1, a gene required for nuclear transport in yeast.  
A;Reference number: A46417; MUID:93066237; PMID:1332047  
A;Accession: A46417  
A;Molecule type: DNA  
A;Residues: 1-812 <GUL>  
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:I02899  
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)  
R;Connor, R.; Churcher, C.W.  
submitted to the EMBL Data Library, April 1995  
A;Reference number: S53969  
A;Accession: S53979  
A;Molecule type: DNA  
A;Residues: 571-592, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>  
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:Y  
R;Churcher, C.W.  
submitted to the EMBL Data Library, September 1995  
A;Reference number: S59302  
A;Accession: S59302  
A;Molecule type: DNA  
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>  
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS:Y  
A;Experimental source: strain AB972

## C;Genetics:

A;Gene: SGD:NIP1  
A;Cross-references: SGD:S0004926; MIPS:YMR309C  
A;Map position: 13R

Query Match 43.9%; Score 43; DB 2; Length 812;  
Best Local Similarity 53.8%; Pred. No. 66;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFI 13

||| ||| : ||| |||  
::|||::|:

Db 361 GVKRLGSIKFSFV 373

## RESULT 12

T04583

TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C;Accession: T04583; T05507

R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T. submitted to the Protein Sequence Database, March 1998

A;Reference number: Z15378

A;Accession: T04583

A;Molecule type: DNA

A;Residues: 1-1607 <BEV>

A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141

A;Experimental source: cultivar Columbia; BAC clone F23E13

R;Bevan, M.; Wedler, H.; Wambutt, R.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelke submitted to the Protein Sequence Database, April 1998

A;Reference number: Z15418

A;Accession: T05507

A;Molecule type: DNA

A;Residues: 1448-1607 <BE2>

A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373

A;Experimental source: cultivar Columbia; BAC clone T19K4

C;Genetics:

A;Map position: 4

A;Intons: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3

A;Note: F23E13.30; T19K4.270

Query Match 43.9%; Score 43; DB 2; Length 1607;  
Best Local Similarity 72.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIRFIRAF 16

||| ||| ||| |||

Db 1321 LGSIRLIRGF 1331

## RESULT 13

T12085

reverse transcriptase homolog - fava bean (fragment)

C;Species: Vicia faba (fava bean)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T12085

R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.

submitted to the EMBL Data Library, September 1997

A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.

A;Reference number: Z17406

A;Accession: T12085

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-407 <KIN>

A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000AAD3D; EMBL:AB007466; NID:d1170509;

A;Experimental source: guard cell protoplasts

C;Superfamily: pol polyprotein

Query Match 43.4%; Score 42.5; DB 2; Length 407;  
Best Local Similarity 57.9%; Pred. No. 40;  
Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GIRFLGSIW--RFIRAF 16

Db 178 GIRFLGHVGFYRRFIRDF 196

||| ||| : ||| |||

## RESULT 14

E84953

penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002

C;Accession: E84953

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: E84953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-760 <STO>

A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mrcB; BU200

C;Superfamily: penicillin-binding protein 1B

Query Match 43.4%; Score 42.5; DB 2; Length 760;  
Best Local Similarity 44.4%; Pred. No. 74;  
Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFL-GSIWRFIRAFYG 18

||| : ||| : |||

Db 32 INRFNGKWNFPFTSIYG 49

## RESULT 15

T52113

probable transcription co-activator KIWI [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C;Accession: T52113

R;Cormack, R.S.; Hahlbrock, K.; Somssich, I.E.

Plant J. 14, 685-92, 1998

A;Title: Isolation of putative plant transcriptional coactivators using a modified two-h

A;Reference number: Z25848; MUID:98346011; PMID:9681033

A;Accession: T52113

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-107 <COR>

A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.1

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: KIWI

A;Map position: V

C;Function:

A;Description: probably plays a role in gene activation during pathogen defence and plant

C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match 42.9%; Score 42; DB 2; Length 107;  
Best Local Similarity 50.0%; Pred. No. 13;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17

||| : ||| |||

Db 54 VRNNGKIWDIREFY 69

Search completed: May 19, 2006, 14:39:58

Job time : 14.2857 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds  
(without alignments)

144.247 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYV 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	Q3APY5_CHLCH	Q3apY5 chlorobium
2	54	55.1	670	Q25271_LEPDE	Q25271 leptinotars
3	52	53.1	735	Q9F7V7_RHILV	Q9f7v7 rhizobium 1
4	52	53.1	805	Q44QD1_CHLLI	Q44qdl chlorobium
5	52	53.1	816	Q43K01_CHLBS	Q43k01 chlorobium
6	51	52.0	407	Q39L57_BURS3	Q39l57 burkholderi
7	51	52.0	408	Q456F4_9BURK	Q456f4 burkholderi
8	51	52.0	408	Q4LK44_9BURK	Q4lk44 burkholderi
9	50	51.0	579	1_XKR7_HUMAN	Q5gh72 homo sapien
10	50	51.0	579	1_XKR7_PANTR	Q49lei pan troglod
11	50	51.0	580	1_XKR7_MOUSE	Q5gh64 mus musculu
12	50	51.0	580	1_XKR7_RAT	Q5gh56 rattus norv
13	49	50.0	409	Q4BFM2_BURVI	Q4bfm2 burkholderi
14	49	50.0	449	Q3PK79_PARDE	Q3pk79 paracoccus
15	49	50.0	488	Q84ZWI_PEA	Q84zwl pisum sativ
16	48	49.0	188	Q2ILN7_9DELT	Q2iln7 anaeromyxob
17	48	49.0	298	Q8R587_MOUSE	Q8r587 mus musculu
18	48	49.0	435	Q2JIT0_9CYAN	Q2jito cyanobacter
19	48	49.0	578	1_XKR6_TETNG	Q49l88 tetraodon n
20	48	49.0	578	Q5GH49_FUGRU	Q5gh49 fugu rubrip
21	48	49.0	627	P74489_SVNY3	P74489 synecocyst
22	47.5	48.5	240	P97035_HAESO	P97035 haemophilus
23	47.5	48.5	577	Q36XB4_RHOPA	Q36xb4 rhodospseudo
24	47.5	48.5	577	Q37C12_RHOPA	Q37c12 rhodospseudo
25	47.5	48.5	807	Q3VMG0_9CHLB	Q3vmg0 pelodicicton
26	47	48.0	486	Q5U414_XENLA	Q5u414 xenopus lae
27	47	48.0	487	Q32N49_XENLA	Q32n49 xenopus lae
28	47	48.0	910	Q2ZDS6_ORYSA	Q2zds6 oryza sativ
29	46	46.9	361	Q2NUB5_SODGL	Q2nub5 sodalis glo
30	46	46.9	385	Q5ZPA2_9DELT	Q5zpa2 angiococcus
31	46	46.9	540	Q5GH65_MOUSE	Q5gh65 mus musculu

32 46 46.9 580 2 Q5GH40\_BRAHE  
33 46 46.9 638 1 XKR6\_RAT  
34 46 46.9 641 1 XKR6\_HUMAN  
35 46 46.9 807 1 SYL\_CHLTE  
36 46 46.9 836 2 Q2Y8V4\_NITMU  
37 46 46.9 859 2 Q3XW00\_MAGNETOCOC  
38 46 46.9 863 2 Q2S415\_9SPHI  
39 46 46.9 2484 2 Q5CEP27\_CRYPV  
40 45 45.9 178 2 Q9RYR0\_DEIRA  
41 45 45.9 219 2 Q6LIT5\_PICTO  
42 45 45.9 276 2 Q4BS81\_BURVI  
43 45 45.9 278 2 Q7VV93\_BORPE  
44 45 45.9 278 2 Q7W7P3\_BORPA  
45 45 45.9 278 2 Q7WL31\_BORBR

#### ALIGNMENTS

RESULT 1  
Q3APY5\_CHLCH  
ID Q3APY5\_CHLCH PRELIMINARY; PRT; 805 AA.  
AC Q3APY5\_2005, integrated into UniProtKB/TrEMBL.  
DT 22-NOV-2005, sequence version 1.  
DT 21-FEB-2006, entry version 5.  
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).  
GN OrderedLocusNames=Cag\_1688;  
OS Chlorobium chlorochromatii (strain Cad3).  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium/Felodictyon group; Chlorobium.  
OX NCBI\_TaxID=340177;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RG US DOE Joint Genome Institute;  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
RA Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F.,  
RA Land M., Kyrpides N., Ivanova N., Richardson P.;  
RT "Complete sequence of Chlorobium chlorochromatii Cad3.";  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License

-----  
EMBL; CP000108; AB28940.1; -; Genomic\_DNA.  
CC GO: 0005324; F:ATP binding; IEA.  
DR GO: 0004823; F:leucine-tRNA ligase activity; IEA.  
DR GO: 0016874; F:ligase activity; IEA.  
DR GO: 0006429; P:leucyl-tRNA aminoacylation; IEA.  
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.  
SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;

Best Local Similarity 69.2%; Pred.No. 3.2; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 2;

Qy 1 GIRRFLGSIWRFI 13

||| ||||| |||||

Db 622 GISRFLGKVRFFV 634

#### RESULT 2

Q25271\_LEPDE

ID Q25271\_LEPDE PRELIMINARY; PRT; 670 AA.

AC Q25271\_1996, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 25.

DE Diapause protein 1 (Fragment).

GN Name=Dp19;

OS Leptinotarsa decemlineata (Colorado potato beetle).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;



ID	Q39L57_BURS3	PRELIMINARY;	PRT;	407 AA.
AC	Q39L57;			
DT	22-NOV-2005,	integrated into UniProtKB/TREMBL.		
DT	22-NOV-2005,	sequence version 1.		
DT	21-FEB-2006,	entry version 4.		
DE	Hypothetical protein.			
GN	OrderedLocusNames=Bcep18194_A3207;			
OS	Burkholderia sp. (strain 383)	(Burkholderia cepacia (strain ATCC 17760 / NCIB 9086 / R18194)).		
OS	/ NCIB 9086 / R18194).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC	Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.			
NCBI_TaxID=269483;				
[1]	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
US DOE Joint Genome Institute;				
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Istrani S., Pitluck S., Chain P., Malfatti S., Shin M., Vergez L., Schmutz J., Latimer F., Land M., Kyripides N., Lykidis A., Richardson P.;				
"Complete sequence of chromosome 1 of Burkholderia sp. 383."				
Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.				
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
Distributed under the Creative Commons Attribution-NoDerivs License				
EMBL; CP000151; ABB06809.1; -; Genomic_DNA.				
Complete proteome; Hypothetical protein.				
KW SEQUENCE	407 AA; 45483 MW; 957829B27BCABFC1 CRC64;			
Query Match	52.0%; Score 51; DB 2; Length 407;			
Best Local Similarity	47.1%; Pred. No. 20;			
Matches	8; Conservative	5; Mismatches	4; Indels	0; Gaps
QY	1 GIRFELGSIWRIFAFY 17			
Db	::  :: :			
	327 GIRQMGLGHVQWTRSSY 343			
RESULT 7				
ID	Q456F4_9BURK	PRELIMINARY;	PRT;	408 AA.
AC	Q456F4;			
DT	13-SEP-2005,	integrated into UniProtKB/TREMBL.		
DT	13-SEP-2005,	sequence version 1.		
DT	07-FEB-2006,	entry version 2.		
DE	Hypothetical protein.			
GN	ORFNames=BcenDRAFT_3751;			
OS	Burkholderia cenocepacia AU 1054.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC	Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.			
NCBI_TaxID=331271;				
[1]	NUCLEOTIDE SEQUENCE.			
RN STRAIN=AU 1054;				
US DOE Joint Genome Institute (JGI-PGF);				
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Istrani S., Pitluck S., Richardson P.;				
"Sequencing of the draft genome assembly of Burkholderia cenocepacia AU 1054."				
Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.				
[2]	NUCLEOTIDE SEQUENCE.			
RN STRAIN=AU 1054;				
US DOE Joint Genome Institute (JGI-ORN);				
Larimer F., Land M.;				
"Annotation of the draft genome assembly of Burkholderia cenocepacia AU 1054."				
Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.				
-! CAUTION: The sequence shown here is derived from an				
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.				
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GN	Name=XXR7; Synonyms=C2OorfL59, XXRG7;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
NCBI	_TaxID=9606;
RN	[1]
RX	NUCLEOTIDE SEQUENCE [MRNA].
RP	Huang C.-H., Chen Y.;
RT	"A superfamily of XK-related genes (XRG) widely expressed in
RT	vertebrates and invertebrates.";
RL	Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RX	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RT	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RT	Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RT	Bailey J.P., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RT	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RT	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RT	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RT	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RT	Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RT	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RT	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RT	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RT	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RT	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RT	Lehvasaaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RT	Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RT	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RT	Olivier K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RT	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RT	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RT	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RT	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RT	Tracey A.C., Tromans A.C., Vaubin M., Wall M., Wallis J.M.,
RT	Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RT	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RT	Rogers J.;
RT	"The DNA sequence and comparative analysis of human chromosome 20.";
RT	Nature 414:855-871(2001).
CC	-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC	(Potential).
CC	-!- SIMILARITY: Belongs to the XK family.
CC	-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC	gene model prediction.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; AY534245; AAOT07094.1; -; mRNA.
DR	EMBL; AL031658; CAB88102.1; ALT SEQ; Genomic_DNA.
DR	Ensembl; ENSG0000101321; Homo sapiens.
DR	HGNC; HGNC:23062; XKR7
KW	Membrane; Transmembrane.
FT	CHAIN
FT	1 579
FT	XK-related protein 7.
FT	/FTID=PRO_0000190788.
FT	Potential.
FT	TRANSMEM 59 79
FT	Potential.
FT	TRANSMEM 89 109
FT	Potential.
FT	TRANSMEM 260 280
FT	Potential.
FT	TRANSMEM 314 334
FT	Potential.
FT	TRANSMEM 355 375
FT	Potential.
FT	TRANSMEM 384 404
FT	Potential.
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Query Match 51.0%; Score 50; DB 1; Length 579;	
Best Local Similarity 58.3%; Pred. No. 42;	
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps	
6 LGSIWRFIARYF 17	
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QY	





Query Match 51.0%; Score 50; DB 1; Length 580;  
 Best Local Similarity 58.3%; Pred. No. 42;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSIRWFIRAFY 17  
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 DB 190 LGQWRYLRALY 201

RESULT 13  
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 AC Q4BFM2; integrated into UniProtKB/TrEMBL.  
 DT 13-SEP-2005, sequence version 1.  
 DT 13-SEP-2005, entry version 2.  
 DE Hypothetical protein.  
 GN ORFNames=Bcep1808DRAFT\_3388;  
 OS Burkholderia vietnamiensis G4.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.  
 OX NCBI\_TaxID=269482;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=G4;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 RA Hammon N., Istrani S., Pitluck S., Richardson P.,  
 RT "Sequencing of the draft genome and assembly of Burkholderia  
 RT vietnamiensis G4";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=G4;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 RA Hammon N., Istrani S., Pitluck S., Richardson P.,  
 RT "Sequencing of the draft genome and assembly of Burkholderia  
 RT vietnamiensis G4";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=G4;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 RA Hammon N., Istrani S., Pitluck S., Richardson P.,  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

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 DB 329 GVREMLGHVQWTRSSY 345

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 AC Q3PK79;  
 DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 25-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.  
 DE Cytochrome P450.  
 GN ORFNames=PdenDRAFT\_4722;  
 OS Paracoccus denitrificans PD1222.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Paracoccus.  
 OX NCBI\_TaxID=318586;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PD1222;  
 RG US DOE Joint Genome Institute (JGI-PGF);  
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,  
 RA Hammon N., Istrani S., Pitluck S., Richardson P.,  
 RT "Sequencing of the draft genome and assembly of Paracoccus  
 RT denitrificans PD1222";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PD1222;  
 RG US DOE Joint Genome Institute (JGI-ORNL);  
 RA Larimer F., Land M.,  
 RT "Annotation of the draft genome assembly of Paracoccus denitrificans  
 RT PD1222";  
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
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DR EMBL; AAIT01000001; FAN68115.1; -; Genomic\_DNA.  
 DR GO; GO:0020037; F:heme binding; IEA.  
 DR GO; GO:0005506; F:iron ion binding; IEA.  
 DR GO; GO:0046872; F:metal ion binding; IEA.  
 DR GO; GO:0004497; F:monooxygenase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR InterPro; IPR002401; EP4501.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00463; EP4501.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN 1.  
 KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.  
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Query Match 50.0%; Score 49; DB 2; Length 449;  
 Best Local Similarity 64.3%; Pred. No. 46;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRLFGSIWRFIRAF 16  
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 DB 9 RQGRGSIWRFIRDF 22

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 AC Q84ZW1;  
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 21.  
 DE Ent-kaurenoic acid oxidase.  
 GN Name=KAO1;  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Shoot;

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RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenic acid oxidase.";
RL Plant Physiol. 131:335-344(2003).
CC -|- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -|- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF537321; AA023063.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR01128; Cytochrome_P450.
DR InterPro; IPR02401; EP4501.
DR PANTHER; PTHR19383; Cytochrome_P450; 1.
DR Pfam; PF00067; P450; 2.
DR PRINTS; PR00463; EP4501.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
DR Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

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Query Match          50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred.No. 50;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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|:|:| |:|
Db      54  FIGNWSFLRAF 65

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Job time : 115.429 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds  
(without alignments)  
63.384 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*
- 1: /EMC Celleria\_SIDS3/ptodata/2/iaa/5 COMB.pep.\*
  - 2: /EMC Celleria\_SIDS3/ptodata/2/iaa/6 COMB.pep.\*
  - 3: /EMC Celleria\_SIDS3/ptodata/2/iaa/7 COMB.pep.\*
  - 4: /EMC Celleria\_SIDS3/ptodata/2/iaa/H COMB.pep.\*
  - 5: /EMC Celleria\_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.\*
  - 6: /EMC Celleria\_SIDS3/ptodata/2/iaa/RE COMB.pep.\*
  - 7: /EMC Celleria\_SIDS3/ptodata/2/iaa/backfileseq.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	79.6	18	2	US-08-940-095-242
2	78	79.6	18	2	US-08-940-093-242
3	78	79.6	18	2	US-08-940-096-242
4	78	79.6	18	2	US-09-465-719-242
5	78	79.6	18	2	US-09-453-605-242
6	78	79.6	18	2	US-09-453-838-242
7	78	79.6	18	2	US-08-940-136-242
8	78	79.6	18	2	US-09-453-841-242
9	78	79.6	18	2	US-09-453-826-242
10	78	79.6	18	2	US-09-453-840-242
11	78	79.6	18	2	US-09-865-989-242
12	78	79.6	18	2	US-09-453-834-242
13	78	79.6	18	2	US-10-283-599-242
14	78	79.6	18	2	US-09-465-718-242
15	78	79.6	18	2	US-09-205-258-892
16	51	52.0	76	2	US-10-004-860-892
17	51	52.0	76	2	US-09-586-106D-49
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22	45	45.9	22	1	US-08-338-882-41
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24	45	45.9	539	2	US-09-710-279-340
25	45	45.9	835	2	US-09-134-001C-5105
26	45	45.9	877	2	US-09-328-352-8162

27	44	44.9	22	1	US-08-132-767-50	Sequence 50, Appl
28	44	44.9	589	1	US-08-756-317-5	Sequence 5, Appl
29	44	44.9	1052	2	US-09-134-000C-6620	Sequence 620, Ap
30	43	43.9	23	3	US-10-360-101-83	Sequence 83, Appl
31	43	43.9	413	3	US-09-609-146-27	Sequence 27, Appl
32	43	43.9	439	3	US-09-609-146-29	Sequence 29, Appl
33	43	43.9	683	2	US-09-502-540-15932	Sequence 15932, A
34	43	43.9	702	2	US-10-094-749-2262	Sequence 2262, Ap
35	43	43.9	812	2	US-09-538-092-643	Sequence 643, Appl
36	42	42.9	14	1	US-08-480-190-3	Sequence 3, Appl
37	42	42.9	14	1	US-08-488-379-3	Sequence 3, Appl
38	42	42.9	14	2	US-08-475-399A-3	Sequence 3, Appl
39	42	42.9	14	2	US-08-077-255A-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1  
US-08-940-095-242  
; Sequence 242, Application US/08940095  
; Patent No. 6004925  
; GENERAL INFORMATION:  
; APPLICANT: Daseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Butner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,095  
; FILING DATE: 29-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cortuzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5856  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6004925e  
US-08-940-095-242

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Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFVG 18
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Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFVG 18
   ||:|||||:|:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

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; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFVG 18
   ||:|||||:|:~|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

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US-09-453-838-242
Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18
   ||::|||:||||:||||:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 7
US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER: US/08/940,136
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18
   ||::|||:||||:||||:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
US-09-453-841-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFYG 18
   ||::|||:||||:||||:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 9
US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```



; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/453,833  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/940,095  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6602854e  
; US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18  
||:|||||:|:|  
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 10  
US-09-453-826-242  
; Sequence 242, Application US/09453826  
; Patent No. 6630450  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/453,826  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/940,095  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6630450e  
; US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18  
||:|||||:|:|  
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 11  
US-09-453-840-242  
; Sequence 242, Application US/09453840  
; Patent No. 6716816  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/453,840  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/940,095  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
US-09-453-834-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

;; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFVG 18

|||||:|:|:|

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

Sequence 242, Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718

;; FILING DATE: 17-Dec-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/940,096

;; FILING DATE: 29-SEP-1997

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

US-09-465-718-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFVG 18

|||||:|:|:|

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55

Job time : 24.8571 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds  
(without alignments)  
102.575 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28	84	85.7	18	4	US-10-712-447-22
29	84	85.7	18	4	US-10-712-447-78
30	84	85.7	18	4	US-10-712-447-95
31	84	85.7	18	4	US-10-712-447-120
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33	82	83.7	18	4	US-10-712-447-56
34	82	83.7	18	4	US-10-712-447-58
35	82	83.7	18	4	US-10-712-447-77
36	82	83.7	18	4	US-10-712-447-79
37	82	83.7	18	4	US-10-712-447-80
38	82	83.7	18	4	US-10-712-447-94
39	81	82.7	18	4	US-10-712-447-57
40	81	82.7	18	4	US-10-712-447-100
41	80	81.6	18	4	US-10-712-447-41
42	79	80.6	18	4	US-10-712-447-97
43	78	79.6	18	3	US-09-865-989-242
44	78	79.6	18	3	US-09-865-989-242
45	78	79.6	18	4	US-10-099-574A-242

#### ALIGNMENTS

##### RESULT 1

US-10-712-447-2  
Sequence 2, Application US/10712447  
Publication No. US20040186057A1  
GENERAL INFORMATION:  
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
APPLICANT: GABER, DAVID W.  
APPLICANT: DATTA, GEETA  
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
FILE REFERENCE: 112739-123US  
CURRENT APPLICATION NUMBER: US/10/712,447  
CURRENT FILING DATE: 2003-11-13  
PRIOR APPLICATION NUMBER: 60/425,821  
PRIOR FILING DATE: 2002-11-13  
NUMBER OF SEQ ID NOS: 210  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 2  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: c-term amidated  
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GIRFLGSIWRFIRAFYG 18

Db 1 GIRFLGSIWRFIRAFYG 18

##### RESULT 2

US-10-712-447-5  
Sequence 5, Application US/10712447  
Publication No. US20040186057A1  
GENERAL INFORMATION:  
APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
APPLICANT: GABER, DAVID W.  
APPLICANT: DATTA, GEETA  
TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
FILE REFERENCE: 112739-123US  
CURRENT APPLICATION NUMBER: US/10/712,447  
CURRENT FILING DATE: 2003-11-13

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; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRRFLGSIWRFIRAFYG 18
Db      1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRRFLGSIWRFIRAFYG 18
Db      1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRRFLGSIWRFIRAFYG 18
Db      1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRRFLGSIWRFIRAFYG 18
Db      1 GRRFLGSIWRFIRAFYG 18
|||||

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-91

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRRFLGSIWRFIRAFYG 18
Db      1 GRRFLGSIWRFIRAFYG 18
|||||
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Tue May 23 08:38:01 2006

OTHER INFORMATION: peptide  
US-10-712-447-74

Query Match 93.9%; Score 92; DB 4; Length 18;  
Best Local Similarity 88.9%; Pred. No. 7.9e-07;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 15  
US-10-712-447-4  
; Sequence 4, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 4  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-4

Query Match 91.8%; Score 90; DB 4; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.6e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 15:27:57  
Job time : 81.2857 secs

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; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-242-505A-18

Query Match      37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRRFLGSIW 10
   :|||:||:|
Db 155 VRRVLGAV 163

RESULT 3
US-09-949-925-142
; Sequence 142, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142
```

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Query Match      37.2%; Score 36.5; DB 1; Length 60;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 FLGSIWRIFAFY 18
   ||:|:|:|
Db 31 FLILVWIFV-AFY 43

RESULT 4
US-09-949-925-111
; Sequence 111, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match      36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWR 12
   :|:|:|
Db 59 LREVSGKIWR 69

RESULT 5
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 5089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM_OMNI
; US-11-302-678-5
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; CURRENT APPLICATION NUMBER: US/11/302,678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-302-678-5

Query Match 36.7%; Score 36; DB 7; Length 599;  
Best Local Similarity 71.4%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LGSWRF 12  
Db 64 LGSWRF 70

RESULT 6  
US-11-242-505A-48  
; Sequence 48, Application US/11242505A  
; Publication No. US2006009656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
; FILE REFERENCE: MPI2001-288PRCPIOMNIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;  
Best Local Similarity 50.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 17

Db 195 LEEAWFLDAFY 206

RESULT 7  
US-10-511-937-2540  
; Sequence 2540, Application US/10511937  
; Publication No. US20060088836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2540  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2540

Query Match 34.7%; Score 34; DB 6; Length 351;  
Best Local Similarity 46.2%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 18  
Db 263 LGIVLKEMLFYG 275

RESULT 8  
US-10-975-692-2  
; Sequence 2, Application US/10975692  
; Publication No. US20060090221A1  
; GENERAL INFORMATION:  
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION  
; APPLICANT: Browne, John A.  
; APPLICANT: Wallis, James G.  
; APPLICANT: Watts, Jennifer L.  
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS  
; FILE REFERENCE: 4630-58963-02  
; CURRENT APPLICATION NUMBER: US/10/975,692  
; CURRENT FILING DATE: 2004-10-26  
; PRIOR APPLICATION NUMBER: US 09/857,583  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/28655  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/111,301  
; PRIOR FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;  
Best Local Similarity 43.8%; Pred. No. 59;  
Matches 7; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 IRRFGLSIWFIKAFY 17  
DB 130 IRKLEITIFLAFY 145

RESULT 9  
US-10-505-928-543  
; Sequence 543, Application US/10505928  
; Publication No. US2006008532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 543  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;  
Best Local Similarity 47.1%; Pred. No. 70;  
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 3 RREF--GSIWRFIRAFY 17  
DB 473 RRFQSGDLVHIRKHF 489

RESULT 10  
US-11-169-140-109  
; Sequence 109, Application US/11169140  
; Publication No. US20060099150A1  
; GENERAL INFORMATION:  
; APPLICANT: ARIZKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou, L.  
; APPLICANT: SHERIDAN, Philip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven  
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE  
; TITLE OF INVENTION: BARRIERS  
; FILE REFERENCE: 11474-037-999  
; CURRENT FILING DATE: 2005-06-27  
; PRIOR APPLICATION NUMBER: US/11/169,140  
; PRIOR FILING DATE: 2005-06-27  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/949,039  
; PRIOR FILING DATE: 2001-09-06  
; PRIOR APPLICATION NUMBER: 09/969,748  
; PRIOR FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 109  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Simian  
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;  
Best Local Similarity 42.1%; Pred. No. 35;  
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 GIRFLGSIW----RPIR 14  
DB 158 GLVLGAVWCVARARFIR 176

RESULT 11  
US-11-204-427-7  
; Sequence 7, Application US/11204427  
; Publication No. US20060100146A1  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L  
; APPLICANT: Turkish, Aaron R  
; APPLICANT: Billheimer, Jeffrey T  
; APPLICANT: Cromley, Debra  
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES  
; FILE REFERENCE: 0575/72796/JPM/AJM/JCS  
; CURRENT APPLICATION NUMBER: US/11/204,427  
; CURRENT FILING DATE: 2005-08-15  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17  
DB 84 AIWRQLRDYY 93

RESULT 12  
US-11-304-129-40  
; Sequence 40, Application US/11304129  
; Publication No. US20060088915A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: TAKATSU, Yoshihiro  
; APPLICANT: WATANABE, Takuya  
; APPLICANT: TERAQ, Yasuko  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: HINUMA, Syuji  
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
; FILE REFERENCE: 2762USOP  
; CURRENT APPLICATION NUMBER: US/11/304,129  
; CURRENT FILING DATE: 2005-12-15  
; PRIOR APPLICATION NUMBER: US/10/333,192  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: JP 2000-217442  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: JP 2001-26779  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 40  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Rat  
US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;  
Best Local Similarity 46.2%; Pred. No. 75;

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Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17
Db 216 FCGQIWPVDQQFY 228

RESULT 13
US-11-304-129-48
; Sequence 48, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAU, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; PRIOR FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 48
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mouse
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17
Db 216 FCGQIWPVDQQFY 228

RESULT 14
US-10-505-928-545
; Sequence 545, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 545
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;
Best Local Similarity 33.3%; Pred. No. 90;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 RFLGSIWRFIRAFY 18
| : : : |
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Db 339 RYYSSBYHYVGGPYG 353

RESULT 15
US-10-505-928-853
; Sequence 853, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 853
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17
| : : : |
Db 1122 LGLIYFVQRFY 1133

Search completed: May 19, 2006, 15:28:18
Job time : 2.14286 secs
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**This Page Blank (uspto)**



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds  
(without alignments)

87.287 Million cell updates/sec

Title: US-10-712-447-10

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYX 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_8.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*
- 10: geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	98	100.0	18	ADO34231	Ado34231 Synthetic
2	98	100.0	18	ADO34225	Ado34225 Synthetic
3	98	100.0	18	ADO34228	Ado34228 Synthetic
4	98	100.0	18	ADO34236	Ado34236 Synthetic
5	98	100.0	18	ADO34233	Ado34233 Synthetic
6	95	96.9	18	ADO34314	Ado34314 Synthetic
7	94	95.9	18	ADO34354	Ado34354 Synthetic
8	94	95.9	18	ADO34338	Ado34338 Synthetic
9	94	95.9	18	ADO34352	Ado34352 Synthetic
10	94	95.9	18	ADO34340	Ado34340 Synthetic
11	94	95.9	18	ADO34339	Ado34339 Synthetic
12	92	93.9	18	ADO34297	Ado34297 Synthetic
13	92	93.9	18	ADO34244	Ado34244 Synthetic
14	92	93.9	18	ADO34276	Ado34276 Synthetic
15	90	91.8	18	ADO34227	Ado34227 Synthetic
16	90	91.8	18	ADO34350	Ado34350 Synthetic
17	89	90.8	18	ADO34322	Ado34322 Synthetic
18	88	89.8	18	ADO34326	Ado34326 Synthetic
19	88	89.8	18	ADO34335	Ado34335 Synthetic
20	88	89.8	18	ADO34337	Ado34337 Synthetic
21	88	89.8	18	ADO34241	Ado34241 Synthetic
22	87	88.8	18	ADO34240	Ado34240 Synthetic
23	86	87.8	18	ADO34284	Ado34284 Synthetic

24	86	87.8	18	ADO34305	Ado34305 Synthetic
25	85	86.7	18	ADO34239	Ado34239 Synthetic
26	85	86.7	18	ADO34344	Ado34344 Synthetic
27	85	86.7	18	ADO34319	Ado34319 Synthetic
28	84	85.7	18	ADO34245	Ado34245 Synthetic
29	84	85.7	18	ADO34301	Ado34301 Synthetic
30	84	85.7	18	ADO34343	Ado34343 Synthetic
31	84	85.7	18	ADO34318	Ado34318 Synthetic
32	82	83.7	18	ADO34302	Ado34302 Synthetic
33	82	83.7	18	ADO34279	Ado34279 Synthetic
34	82	83.7	18	ADO34303	Ado34303 Synthetic
35	82	83.7	18	ADO34242	Ado34242 Synthetic
36	82	83.7	18	ADO34300	Ado34300 Synthetic
37	82	83.7	18	ADO34281	Ado34281 Synthetic
38	82	83.7	18	ADO34317	Ado34317 Synthetic
39	81	82.7	18	ADO34323	Ado34323 Synthetic
40	81	82.7	18	ADO34280	Ado34280 Synthetic
41	80	81.6	18	ADO34264	Ado34264 Synthetic
42	79	80.6	18	ADO34320	Ado34320 Synthetic
43	78	79.6	18	AA18917	Aay18917 Lecithin:
44	78	79.6	18	AA19171	Aay19171 Lecithin:
45	78	79.6	18	AA19425	Aay19425 Lecithin:

#### ALIGNMENTS

##### RESULT 1

ID ADO34231 standard; peptide; 18 AA.

XX ADO34231;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
CC polypeptide. The invention further comprises an isolated nucleic acid  
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
CC a host cell, a recombinant cell or a transgenic, non-human subject  
CC (including animal or plant) comprising the synthetic apolipoprotein-E  
CC mimicking polypeptide encoding polynucleotide; a composition comprising  
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease.  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
 SQ  
 Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRIFAFYG 18  
 Db 1 GIRRFLGSIWRIFAFYG 18  
 |||||

RESULT 2  
 ADO34225  
 ID ADO34225 standard; peptide; 18 AA.

XX ADO34225;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 18

FT /note= "C-terminal amide"

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 2; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRIFAFYG 18  
 Db 1 GIRRFLGSIWRIFAFYG 18  
 |||||

RESULT 3  
 ADO34228  
 ID ADO34228 standard; peptide; 18 AA.

XX ADO34228;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 5; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 4

ADO34236  
 ID ADO34236 standard; peptide; 18 AA.

XX AC ADO34236;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 13; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 5

ADO34233

ID ADO34233 standard; peptide; 18 AA.

XX AC ADO34233;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 10; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRIFAFYVG 18  
 |||:|||||  
 Db 1 GIRRFLGSIWRIFAFYVG 18

RESULT 6  
 ADO34314  
 ID ADO34314 standard; peptide; 18 AA.

XX  
 AC ADO34314;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 91; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRIFAFYVG 18  
 |||:|||||  
 Db 1 GIRRFLGSIWRIFAFYVG 18

RESULT 7  
 ADO34354  
 ID ADO34354 standard; peptide; 18 AA.

XX  
 AC ADO34354;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 131; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
 SQ

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8  
 ADO34338  
 ID ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 115; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;  
 SQ

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9  
 ADO34352  
 ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 129.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 129; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYVG 18  
 |||||:||||:  
 Db 1 GIRRFGLSLWRFIRAFYVG 18

# RESULT 10

ADO34340  
 ID ADO34340 standard; peptide; 18 AA.

XX AC ADO34340;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 117; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYVG 18  
 |||||:||||:  
 Db 1 GIRRFGLSIWRFIRAFYVG 18

# RESULT 11

ADO34339  
 ID ADO34339 standard; peptide; 18 AA.

XX AC ADO34339;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 116; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is



CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYV 18  
 |||||:|||||:|||||  
 Db 1 GIRFLGAIWRFIRSFYV 18

RESULT 14  
 ADO34276  
 ID ADO34276 standard; peptide; 18 AA.

AC ADO34276;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.

KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

Key Location/Qualifiers

Modified-site 1.18 /note= "All Lys residues are DiMethyl-Lysine"

WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYV 18  
 |||||:|||||:|||||  
 Db 1 GIRFLGSIWRFIRAFYV 18

RESULT 15

ADO34227

ID ADO34227 standard; peptide; 18 AA.

AC ADO34227;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking related R18L linear peptide.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein, VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is



CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX  
SQ Sequence 18 AA;  
Query Match 91.8%; Score 90; DB 8; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.1e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GRRFLGSIWRFIRAFYG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:31  
Job time : 94.2857 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds

(without alignments)  
121.233 Million cell updates/sec

Title: US-10-712-447-10

Perfect score: 98

Sequence: 1 GIRRFGLSIWRFIRAFYV 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	2	S76462
2	45	45.9	178	2	A75578
3	44	44.9	461	1	G54537
4	44	44.9	589	2	A34341
5	44	44.9	806	2	A94060
6	44	44.9	861	2	H64102
7	43.5	44.4	1025	2	A93568
8	43	43.9	265	2	T32316
9	43	43.9	489	2	B84733
10	43	43.9	516	2	T33269
11	43	43.9	812	2	A46417
12	43	43.9	1607	2	T04583
13	42.5	43.4	407	2	T12085
14	42.5	43.4	760	2	E84953
15	42	42.9	107	2	T52113
16	42	42.9	214	2	D72540
17	42	42.9	228	2	T15530
18	42	42.9	237	2	B72692
19	42	42.9	246	2	I54412
20	42	42.9	258	2	F71707
21	42	42.9	258	2	D97700
22	42	42.9	273	1	HLHU69
23	42	42.9	365	1	HLHUA2
24	42	42.9	365	2	I38443
25	42	42.9	365	2	I61902
26	42	42.9	365	2	I37542
27	42	42.9	365	2	I84448
28	42	42.9	365	2	I61857
29	42	42.9	365	2	I38442

30	42	42.9	537	2	T04745
31	42	42.9	803	2	AD1282
32	42	42.9	803	2	AH1653
33	42	42.9	804	2	B89961
34	42	42.9	804	2	D69650
35	41.5	42.3	790	2	T50337
36	41	41.8	131	2	AG2115
37	41	41.8	265	2	C42595
38	41	41.8	279	2	E64109
39	41	41.8	359	2	T20575
40	41	41.8	364	2	AF2599
41	41	41.8	364	2	G97381
42	41	41.8	384	2	T08940
43	41	41.8	406	2	F96571
44	41	41.8	503	2	D96776
45	41	41.8	519	1	T02263

hypothetical prote  
leucyl-tRNA synthe  
leucyl-tRNA synthe  
leucyl-tRNA synthe  
leucine-tRNA ligas  
homolog to drosoph  
hypothetical prote  
rfap protein - Esc  
dimethylsulfoxide  
hypothetical prote  
probable parmesane  
hypothetical prote  
hypothetical prote  
hypothetical prote  
cytochrome P450 DW

ALIGNMENTS

RESULT 1

S76462

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C;Species: Synecocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S76462

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

8.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76462

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-627 <KAN>

A;Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID:

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFYV 18

Db 597 GLEQLLGKIQWLQRKFG 614

RESULT 2

A75578

transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: A75578

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: A75578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-178 <WHI>

A;Cross-references: UNIPROT:Q9YR0; UNIPARC:UPI00000D3BE4; GB:AE001863; NID:

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRA0248

A;Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14  
| | | | |  
Db 23 ILRFLGGIWRLLNR 35

RESULT 3  
G64537  
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: G64537  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: G64537  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-461 <TOM>  
A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143  
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14  
: | | | | |  
Db 297 VRLLSWFWRFR 309

RESULT 4  
A34341  
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus  
C;Species: Alcaligenes eutrophus  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34341; A39190  
R;Pocpies, O.P.; Sinskey, A.J.  
J. Biol. Chem. 264, 15298-15303, 1989  
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident  
A;Reference number: A34341; MUID:89359357; PMID:2670936  
A;Accession: A34341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-589 <PEO>  
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:G141958; PIDN:  
R;Schubert, P.; Krueger, N.; Steinbuechel, A.  
J. Bacteriol. 173, 168-175, 1991  
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt  
omoter.  
A;Reference number: A39190; MUID:91100279; PMID:1987116  
A;Accession: A39190  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-219 <SCH>  
A;Cross-references: UNIPARC:UPI000016B162; GB:M64341; NID:G141964; PIDN:AAA21979.1; PID:  
A;Note: the authors translated the codon TAC for residue 120 as Thr  
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC  
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;  
Best Local Similarity 47.6%; Pred. No. 33;  
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RRFLLGSIW-----RFIRAFY 17  
| | | | |

Db 100 RRFAGDAWRTNLPLPYFAAFY 120

RESULT 5  
A84060  
leucyl-tRNA synthetase leus [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: A84060  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: A84060  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-806 <STO>  
A;Cross-references: UNIPROT:Q9K758; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: leus  
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;  
Best Local Similarity 53.8%; Pred. No. 45;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13  
| | | | |  
Db 622 GARRFLDRVWRL 634

RESULT 6  
H64102  
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)  
N;Alternate names: leucyl-tRNA synthetase  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: H64102  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fughmann, J.L.; Goughagen, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: H64102  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-861 <TIGR>  
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:g15;  
C;Genetics:  
A;Gene: leus  
C;Superfamily: leucine-tRNA ligase  
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;  
Best Local Similarity 46.2%; Pred. No. 48;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13  
| | | | |  
Db 665 GAKRFLGRVWNLV 677

RESULT 7  
AH3568  
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AH3568  
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.  
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc

```

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Cross-references: UNIPROT:QBVCQ5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AA153715.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10473
A;Map position: 11
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

Qy 5 FLGSIWRFI---RAFY 17
Db 531 FLGSVNSFWTLPRSF 546

RESULT 8
T32316
hypothetical protein F31F4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32316
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F31F4.
A;Reference number: 221149
A;Accession: T32316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <BLA>
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AA870384.
A;Experimental source: strain Bristol N2; clone F31F4
C;Genetics:
A;Gene: CESP:F31F4.4
A;Map position: 5
A;Introns: 13/3; 67/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFVG 18
Db 253 LASLWAFVHAPEG 265

RESULT 9
B84733
probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009DBED; GB:AE002093; NID:G3831452; PI
C;Genetics:
A;Gene: At2G32440

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A;Map position: 2
C;Superfamily: Synchocystis cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
Db 54 IGNMWSFLRAF 64

RESULT 10
T33269
hypothetical protein C24B9.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AA19257.1
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IRRFLGSIWRFIRAFYG 18
Db 252 LKPFITSLWMFMHAFDG 268

RESULT 11
A46417
NIP1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei
C;Species: Saccharomyces cerevisiae
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S59302
R;Gu, Z.; Moersschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIP1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
A;Accession: A46417
A;Molecule type: DNA
A;Residues: 1-812 <GUL>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
R;Connor, R.; Churcher, C.W.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
A;Molecule type: DNA
A;Residues: 571-582, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:YN
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
A;Molecule type: DNA
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS:YN
A;Experimental source: strain AB972

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C;Genetics:
A;Gene: SGD:N1P1
A;Cross-references: SGD:S0004926; MIPS:YMR309c
A;Map position: 13R

Query Match          43.9%; Score 43; DB 2; Length 812;
Best Local Similarity 53.8%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 0; Indels 2; Gaps 0;

QY 1 GIRFLGSIWRFI 13
    :|||:::|
    361 GVXKILGSIFS FV 373

Db
RESULT 12
T04583
TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04583; T05507
R;Bavan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
submitted to the Protein Sequence Database, March 1998
A;Reference number: 215378
A;Accession: T04583
A;Molecule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: UNIPROT:O65506; UNIPARC:UPI000000AA45C; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
R;Bavan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller
submitted to the Protein Sequence Database, April 1998
A;Reference number: 215418
A;Accession: T05507
A;Molecule type: DNA
A;Residues: 1448-1607 <BE2>
A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetics:
A;Map position: 4
A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270

Query Match          43.9%; Score 43; DB 2; Length 1607;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16
    |||||
    1321 LGSSWRLIRGF 1331

Db
RESULT 13
T12085
reverse transcriptase homolog - fava bean (fragment)
C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Reference number: 217406
A;Accession: T12085
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-407 <KIN>
A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000A0AD3D; EMBL:AB007466; NID:d1170509;
A;Experimental source: guard cell protoplasts
C;Superfamily: pol polyprotein

Query Match          43.4%; Score 42.5; DB 2; Length 407;
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GIRFLGSIW--RFIRAF 16
    |||||
    178 GIRFLGHVGFYRRFIRD 196

Db
RESULT 14
E84953
penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A1
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-760 <STO>
A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: mrcB; BU200
C;Superfamily: penicillin-binding protein 1B

Query Match          43.4%; Score 42.5; DB 2; Length 760;
Best Local Similarity 44.4%; Pred. No. 74;
Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFL-GSIWRFIRAFYG 18
    |||||
    32 INRFINGKWNFTSIYG 49

Db
RESULT 15
T52113
probable transcription co-activator KIWI [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52113
R;Cormack, R.S.; Hahlbrock, K.; Somesich, I.E.
Plant J. 14, 685-92, 1998
A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hy
A;Reference number: Z25848; MUID:98346011; PMID:9681033
A;Accession: T52113
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-107 <COR>
A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.J
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: KIWI
A;Map position: V
C;Function:
A;Description: probably plays a role in gene activation during pathogen defence and plant
C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match          42.9%; Score 42; DB 2; Length 107;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17
    :|||
    54 VRNWGKIWDIREFY 69

Db
Search completed: May 19, 2006, 14:39:59
Job time : 15.2857 secs
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 seconds  
(without alignments)  
144.247 Million cell updates/sec

Title: US-10-712-447-10  
Perfect score: 98  
Sequence: 1 GIRFLGSIWRFAVYG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	2	Q3APV5_CHLCH
2	54	55.1	670	2	Q25271_LEPDE
3	52	53.1	735	2	Q9F7V7_RHILV
4	52	53.1	805	2	Q44QD1_CHLLI
5	52	53.1	816	2	Q43K01_9CHLB
6	51	52.0	407	2	Q39L57_BURS3
7	51	52.0	408	2	Q456F4_9BURK
8	51	52.0	408	2	Q4LK44_9BURK
9	50	51.0	579	1	QXR7_HUMAN
10	50	51.0	579	1	QXR7_PANTR
11	50	51.0	580	1	QXR7_MOUSE
12	50	51.0	580	1	QXR7_RAT
13	49	50.0	409	2	Q4BFM2_BURVI
14	49	50.0	449	2	Q3PK79_PARDE
15	49	50.0	488	2	Q84ZM1_PEA
16	48	49.0	188	2	Q3ILN7_9DELT
17	48	49.0	298	2	Q8R587_MOUSE
18	48	49.0	435	2	Q3JIT0_9CYAN
19	48	49.0	578	1	QXR6_TETNG
20	48	49.0	578	2	Q5GH49_FUGRU
21	48	49.0	627	2	P74489_SYNY3
22	47.5	48.5	240	2	P97035_HAESO
23	47.5	48.5	577	2	Q36XB4_RHOPA
24	47.5	48.5	577	2	Q37C12_RHOPA
25	47.5	48.5	807	2	Q3VMG0_9CHLB
26	47	48.0	486	2	Q5U4I4_XENLA
27	47	48.0	487	2	Q32N49_XENLA
28	47	48.0	910	2	Q5ZDS6_ORYSA
29	46	46.9	361	2	Q2NUB5_SODGL
30	46	46.9	385	2	Q5ZPA2_9DELT
31	46	46.9	540	2	Q5GH65_MOUSE

32 46 46.9 580 2 Q5GH40\_BRARE  
33 46 46.9 638 1 XKR6\_RAT  
34 46 46.9 641 1 XKR6\_HUMAN  
35 46 46.9 807 1 SYL\_CHLTE  
36 46 46.9 836 2 Q2Y8V4\_NITMU  
37 46 46.9 859 2 Q3XW00\_9PROT  
38 46 46.9 863 2 Q2S415\_9SPHI  
39 46 46.9 2484 2 Q5CP27\_CRYPV  
40 45 45.9 178 2 Q9RYR0\_DEIRA  
41 45 45.9 219 2 Q6LIT5\_PICVO  
42 45 45.9 276 2 Q4BS81\_BURVI  
43 45 45.9 278 2 Q7VW93\_BORPE  
44 45 45.9 278 2 Q7W7P3\_BORPA  
45 45 45.9 278 2 Q7WL31\_BORBR

#### ALIGNMENTS

RESULT 1  
Q3APV5\_CHLCH  
ID Q3APV5\_CHLCH PRELIMINARY; PRT; 805 AA.  
AC Q3APV5\_2005, integrated into UniProtKB/TrEMBL.  
DT 22-NOV-2005, sequence version 1.  
DT 21-FEB-2006, entry version 5.  
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).  
GN OrderedLocusNames=Cag\_1688;  
OS Chlorobium chlorochromatii (strain Cad3).  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium/Pelodictyon group; Chlorobium.  
OX NCBI\_TaxID=340177;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RG US DOE Joint Genome Institute; A., Barry K., Dettler J.C., Glavina T.,  
RA Copeland A., Lucas S., Lapidus S., Bryant D., Schmutz J., Larimer F.,  
RA Hammon N., Irani S., Pitluck S., Ivanova N., Richardson P.,  
RA Land M., Kyripides N., Ivanova N., Richardson P.,  
RT "Complete sequence of Chlorobium chlorochromatii Cad3.";  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL: CP000108; ABB28940.1; -; Genomic\_DNA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004823; F:leucine-tRNA ligase activity; IEA.  
DR GO: GO:0016874; F:ligase activity; IEA.  
DR GO: GO:0006429; F:leucyl-tRNA aminoacylation; IEA.  
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.  
SQ SEQUENCE 805 AA; 92007 MW; AOC78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;

Best Local Similarity 69.2%; Pred. No. 3.2; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 2;

Oy 1 GIRFLGSIWRFI 13

Db 622 GISRFLGKWRFFV 634

Qy 1 GIRFLGSIWRFI 13

Db 622 GISRFLGKWRFFV 634

#### RESULT 2

Q25271\_LEPDE PRELIMINARY; PRT; 670 AA.

ID Q25271\_LEPDE PRELIMINARY; PRT; 670 AA.

AC Q25271\_1996, integrated into UniProtKB/TrEMBL.

DT 01-NOV-1996, sequence version 1.

DT 07-FEB-2006, entry version 25.

DE Diapause protein 1 (Fragment).

GN Name=Dp19;

OS Leptinotarsa decemlineata (Colorado potato beetle).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

GO; GO:0015931; P:protein transport; IEA.  
GO; GO:0006508; P:proteolysis; IEA.  
InterPro; IPR003593; AAA\_ATPase.  
InterPro; IPR011527; ABC\_TM\_1.  
InterPro; IPR001140; ABC\_TM\_transp.  
InterPro; IPR003439; ABC\_transp\_like.  
InterPro; IPR005074; Peptidase\_C39.  
InterPro; IPR010132; Type\_I\_sec\_HlyB.  
PANTHER; PTHR19242:SF74; Type\_I\_sec\_HlyB; 1.  
DR Pfam; PF00664; ABC\_membrane; 1.  
DR Pfam; PF00005; ABC\_tran; 1.  
DR Pfam; PF03412; Peptidase\_C39; 1.  
DR ProDom; PD000006; ABC\_transporter; 1.  
DR SMART; SM00382; AAA; 1.  
DR TIGRFAMs; TIGR01846; type\_I\_sec\_HlyB; 1.  
DR PROSITE; PS50929; ABC\_TMIF; 1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.  
DR PROSITE; PS50990; PEPTIDASE\_C39; 1.  
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;  
Best Local Similarity 62.5%; Pred.No. 26;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAF 16  
| | | : | | |  
DB 161 GFHFPLPAWRYRAF 176

RESULT 4  
Q44QD1 CHLLI PRELIMINARY; PRT; 805 AA.  
AC Q44QD1\_  
DT 13-SEP-2005, integrated into UniprotKB/TreMBL.  
DT 13-SEP-2005, sequence version 1.  
DT 11-FEB-2006, entry version 9.  
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.  
OS ORFNAMES=ClimDraft 1980;  
GN Chlorobium limicola DSM 245.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium/Pelodictyon group; Chlorobium.  
NCBI\_TaxId=290315;  
OX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP RP STRAIN=DSM 245;  
RC US DOE Joint Genome Institute (JGI-PGF);  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,  
RA Hammon N., Israni S., Piluck S., Richardson P.;  
RA "Sequencing of the draft genome and assembly of Chlorobium limicola  
RT DSM 245."; R  
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DSM 245;  
RG US DOE Joint Genome Institute (JGI-ORNL);  
RA Larimer F., Land M.;  
RT "Annotation of the draft genome assembly of Chlorobium limicola DSM  
RN 245.";  
CC CC Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

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EMBL: ABXJ01000009; EAM43320.1; -: Genomic\_DNA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.  
DR GO; GO:0006429; F:leucyl-tRNA aminoacylation; IEA.  
DR InterPro; IPR002302; Leu\_tRNAsyn\_la.  
DR Pfam; PF001133; tRNA-synt 1; 1.



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DR PRINTS; PRO0985; TRNASYNTHLEU.
KW TIGRFAMs; TIGR00396; leuS_bact; 1.
SQ SEQUENCE 805 AA; 91997 MW; D4P3FE28P9E92DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFI 13
Db 622 GISRPLGKVMRLV 634

RESULT 5
Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
ID Q43K01_9CHLB
AC Q43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC
CC EMBL; AA1801000002; EAMJ5935.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNAsyn_1a.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leuS_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFI 13
Db 622 GISRPLGKVMRLV 634

RESULT 6
Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
ID Q39L57;
AC Q39L57;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocNames=Scepl8194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; CP000151; AB806809.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFY 17
Db 327 GIROMLGHVQWOTRSSY 343

RESULT 7
Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
ID Q456F4_9BURK
AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=BcendRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC
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Db      190 LGQVRYRLALY 201

RESULT 10
ID_XKR7_PANTR STANDARD; PRT; 579 AA.
AC O49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -----
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CC -----
DR EMBL; AY534253; AAT07102.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
KW Membrane; Transmembrane.
FT CHAIN 1 580
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 303 323
FT TRANSMEM 326 346
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSWRFIRAFY 17
Db      190 LGQVRYRLALY 201

RESULT 12
ID_XKR7_RAT STANDARD; PRT; 580 AA.
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -----
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CC -----
DR EMBL; AY534261; AAT07110.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
KW Membrane; Transmembrane.
FT CHAIN 1 580
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 303 323
FT TRANSMEM 326 346
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;

Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSWRFIRAFY 17
Db      190 LGQVRYRLALY 201

RESULT 11
ID_XKR7_MOUSE STANDARD; PRT; 580 AA.
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
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CC -----
DR EMBL; AY702910; AAV83783.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
KW Membrane; Transmembrane.
FT CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093B5D4 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSWRFIRAFY 17
Db      190 LGQVRYRLALY 201

RESULT 11
ID_XKR7_MOUSE STANDARD; PRT; 580 AA.
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
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CC -----
DR EMBL; AY702910; AAV83783.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
KW Membrane; Transmembrane.
FT CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093B5D4 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSWRFIRAFY 17
Db      190 LGQVRYRLALY 201

RESULT 12
ID_XKR7_RAT STANDARD; PRT; 580 AA.
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -----
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CC -----
DR EMBL; AY534261; AAT07110.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
KW Membrane; Transmembrane.
FT CHAIN 1 580
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 303 323
FT TRANSMEM 326 346
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
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Query Match      51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIRWFIRAFY 17
   ||:|||||
Db 190 LGQWRYRLALY 201

RESULT 13
Q4BPM2_BURVI
ID Q4BPM2_BURVI PRELIMINARY; PRT; 409 AA.
AC Q4BPM2;
DT 13-SEP-2005, integrated into UniprotKB/TREMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcep1808DRAFT_3388;
OS Burkholderia vietnamiensis G4.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=269482;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia vietnamiensis
RT G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC
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DR EMBL; AA02000029; EMBL28562.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 409 AA; 45629 MW; CCD3FA52A9F014E4 CRC64;

Query Match      50.0%; Score 49; DB 2; Length 409;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFY 17
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Db 329 GVREMLGHVQWTRSSY 345

RESULT 14
Q3PK79_PARDE
ID Q3PK79_PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniprotKB/TREMBL.
DT 25-OCT-2005, sequence version 1.

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DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
GN ORFNames=PdenDRAFT_4722;
OS Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OC NCBI_TaxID=318586;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Paracoccus
RT denitrificans PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Paracoccus denitrificans
RT PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC -i- SIMILARITY: Belongs to the cytochrome P450 family.
CC
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DR EMBL; AAIT01000001; EMBL6115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;

Query Match      50.0%; Score 49; DB 2; Length 449;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFGLSIWRFIRAF 16
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Db 9 RQGRGSVWRPIRDF 22

RESULT 15
Q84ZW1_PEA
ID Q84ZW1_PEA PRELIMINARY; PRT; 488 AA.
AC Q84ZW1;
DT 01-JUN-2003, integrated into UniprotKB/TREMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Ent-kaurenoic acid oxidase.
GN Name=KA01;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OC NCBI_TaxID=3888;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Shoot;

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RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;  
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;  
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";  
RL Plant Physiol. 131:335-344(2003).  
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL; AF537321; AA023063.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0020037; F:heme binding; IEA.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0004497; F:monooxygenase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR InterPro; IPR02401; EP450I.  
DR PANTHER; PTHR19383; Cytochrome\_P450; 1.  
DR Pfam; PF00067; P450; 2.  
DR PRINTS; PR00463; EP450I.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN 1.  
KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;  
KW Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;  
Best Local Similarity 58.3%; Pred. No. 50;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAF 16  
|:|:|:|:|:|:|  
Db 54 FIGNWSFLRAF 65

Search completed: May 19, 2006, 14:38:15  
Job time : 116.429 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds  
(without alignments)  
63.384 Million cell updates/sec

Title: US-10-712-447-10

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAPYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pep:\*
  - 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pep:\*
  - 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pep:\*
  - 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pep:\*
  - 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pep:\*
  - 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pep:\*
  - 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	79.6	18	2	US-08-940-095-242
2	78	79.6	18	2	US-08-940-093-242
3	78	79.6	18	2	US-08-940-096-242
4	78	79.6	18	2	US-09-465-719-242
5	78	79.6	18	2	US-09-453-605-242
6	78	79.6	18	2	US-09-453-838-242
7	78	79.6	18	2	US-08-940-136-242
8	78	79.6	18	2	US-09-453-841-242
9	78	79.6	18	2	US-09-453-833-242
10	78	79.6	18	2	US-09-453-826-242
11	78	79.6	18	2	US-09-453-840-242
12	78	79.6	18	2	US-09-865-989-242
13	78	79.6	18	2	US-09-453-834-242
14	78	79.6	18	2	US-10-283-599-242
15	78	79.6	18	2	US-09-465-718-242
16	51	52.0	76	2	US-09-205-258-892
17	51	52.0	76	2	US-10-004-860-892
18	47.5	48.5	253	2	US-09-586-106D-49
19	47.5	48.5	253	2	US-10-799-870-49
20	45.5	46.4	254	2	US-09-586-106D-45
21	45.5	46.4	254	2	US-10-799-870-45
22	45	45.9	22	1	US-08-338-882-40
23	45	45.9	22	1	US-08-338-882-41
24	45	45.9	539	2	US-09-710-279-340
25	45	45.9	835	2	US-09-134-001C-5105
26	45	45.9	877	2	US-09-328-352-8162

27	44	44.9	22	1	US-08-132-767-50	Sequence 50, Appl
28	44	44.9	589	1	US-08-756-317-5	Sequence 5, Appli
29	44	44.9	1052	2	US-09-134-000C-6620	Sequence 6620, Ap
30	43	43.9	23	2	US-10-360-101-83	Sequence 83, Appl
31	43	43.9	413	3	US-09-609-146-27	Sequence 27, Appl
32	43	43.9	439	3	US-09-609-146-29	Sequence 29, Appl
33	43	43.9	683	2	US-09-902-540-15932	Sequence 15932, A
34	43	43.9	702	2	US-10-094-749-2262	Sequence 2262, Ap
35	43	43.9	812	2	US-09-538-092-643	Sequence 643, App
36	42	42.9	14	1	US-08-480-190-3	Sequence 3, Appli
37	42	42.9	14	1	US-08-488-379-3	Sequence 3, Appli
38	42	42.9	14	2	US-08-475-399A-3	Sequence 3, Appli
39	42	42.9	14	2	US-08-077-255A-3	Sequence 3, Appli
40	42	42.9	14	5	PCT-US93-07545-3	Sequence 3, Appli
41	42	42.9	15	1	US-08-480-190-2	Sequence 2, Appli
42	42	42.9	15	1	US-08-488-379-2	Sequence 2, Appli
43	42	42.9	15	2	US-08-475-399A-2	Sequence 2, Appli
44	42	42.9	15	2	US-08-077-255A-2	Sequence 2, Appli
45	42	42.9	15	5	PCT-US93-07545-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-940-095-242  
; Sequence 242, Application US/08940095  
; Patent No. 6004925  
; GENERAL INFORMATION:  
; APPLICANT: Daseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttnet, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,095  
; FILING DATE: 29-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6004925e  
US-08-940-095-242

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Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIKAFVG 18
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Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIKAFVG 18
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Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
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; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIKAFVG 18
   ||:|||||:|:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
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US-09-453-838-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18  
||:|||||:|||||  
Db 1 GIKKFLGSIWKFIKAFVG 18

## RESULT 7

US-08-940-136-242

; Sequence 242, Application US/08940136

; Patent No. 6518412

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: GENE THERAPY APPROACHES TO

; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR

; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/940,136

; FILING DATE: 29-SEP-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0007-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6518412e

US-08-940-136-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18  
||:|||||:|||||  
Db 1 GIKKFLGSIWKFIKAFVG 18

## RESULT 8

US-09-453-841-242

; Sequence 242, Application US/09453841

; Patent No. 6573239

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/453,841

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/940,095

; FILING DATE: 29-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0004-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6573239e

US-09-453-841-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18  
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Db 1 GIKKFLGSIWKFIKAFVG 18

## RESULT 9

US-09-453-833-242

; Sequence 242, Application US/09453833

; Patent No. 6602854

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,833  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6602854e  
US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18  
||:|||||:|:|  
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 10  
US-09-453-826-242  
Sequence 242, Application US/09453826  
Patent No. 6630450  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,826  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6630450e  
US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18  
||:|||||:|:|  
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 11  
US-09-453-840-242  
Sequence 242, Application US/09453840  
Patent No. 6716816  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,840  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18
|:::|||||:|:|

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18
|:::|||||:|:|
```

```
RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
US-09-453-834-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18
|:::|||||:|:|

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

;; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

;; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18

||:|||||:|:|

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

;; Sequence 242, Application US/09465718

;; Patent No. 6900177

;; GENERAL INFORMATION:

;; APPLICANT: Dasseux, Jean-Louis

;; APPLICANT: Sekul, Renate

;; APPLICANT: Buttner, Klaus

;; APPLICANT: Cornut, Isabelle

;; APPLICANT: Metz, Gunther

;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

;; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

;; NUMBER OF SEQUENCES: 258

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718

;; FILING DATE: 17-Dec-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/940,096

;; FILING DATE: 29-SEP-1997

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

;; US-09-465-718-242

Query Match

Best Local Similarity 72.2%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18

||:|||||:|:|

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:56

Job time : 25.8571 secs

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; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
```



```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-91

Query Match          96.9%; Score 95; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GIRKFLGSIWRFIRAFYG 18

RESULT 7
US-10-712-447-115
; Sequence 115, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-115

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 8
US-10-712-447-116
; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 116
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 9
US-10-712-447-117
; Sequence 117, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-117

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   |:|:~:~:~:~:~:~:~:~:~
Db 1 GIRRFIGSIWRFIRAFYG 18

RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-129
```



```
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GIRRFLGSIWRFIRAFYG 18
      |||:|||:|||:|||:|||
Db      1 GIRKFLGSIWRFIRAFYG 18

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4
Query Match      91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GIRRFLGSIWRFIRAFYG 18
      |||:|||:|||:|||:|||
Db      1 GIRRFLGSIWRFIRAFYG 18

Search completed: May 19, 2006, 15:27:57
Job time : 81.2857 secs
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; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58674, 252, 304, 1980, 14717, 9941, 19310,  
; FILE REFERENCE: MPI2001-288PIRCPIONNM  
; CURRENT APPLICATION NUMBER: US/11/242.505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-242-505A-18

Query Match 37.8%; Score 37; DB 7; Length 403;  
Best Local Similarity 55.6%; Pred. No. 16;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRFLGSIW 10  
Db 155 VRRVLGAW 163

RESULT 3  
US-09-949-925-142  
; Sequence 142, Application US/09949925  
; Publication No. US2006009575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 142  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (60)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-949-925-142

Query Match 37.2%; Score 36.5; DB 1; Length 60;  
Best Local Similarity 57.1%; Pred. No. 2.2;  
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 5 FLGSIWRFIRAFY 18  
Db 31 FLILVWIFV-AFY 43

RESULT 4  
US-09-949-925-111  
; Sequence 111, Application US/09949925  
; Publication No. US2006009575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (74)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-949-925-111

Query Match 36.7%; Score 36; DB 1; Length 74;  
Best Local Similarity 54.5%; Pred. No. 3.3;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRFLGSIWRF 12  
Db 59 LREVSGKIMRF 69

RESULT 5  
US-11-302-678-5  
; Sequence 5, Application US/11302678  
; Publication No. US2006008881A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012PIRNM\_OMNI

Db 195 LEEAWSFDAFY 206

RESULT 7

US-10-511-937-2540

; Sequence 2540, Application US/10511937

; Publication No. US2006008836A1

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlseuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT FILING DATE: 2004-10-19

; CURRENT APPLICATION NUMBER: US/10/511.937

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 2540

; LENGTH: 351

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-511-937-2540

Query Match 36.7%; Score 36; DB 7; Length 599;

Best Local Similarity 71.4%; Pred. No. 38;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LGSWRF 12

Db 64 LGNVWF 70

RESULT 6

US-11-242-505A-48

; Sequence 48, Application US/11242505A

; Publication No. US20060099656A1

; GENERAL INFORMATION:

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; TITLE OF INVENTION: Methods and Compositions for Treating

; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,

; FILE REFERENCE: MPI2001-288P10NMIM

; CURRENT FILING DATE: 2005-10-03

; PRIOR FILING DATE: 2005-10-03

; PRIOR APPLICATION NUMBER: US 10/290,078

; PRIOR FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: US 60/347,949

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 10/320,351

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341,606

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 48

; LENGTH: 313

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 17

Query Match 34.7%; Score 34; DB 6; Length 351;

Best Local Similarity 46.2%; Pred. No. 44;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 18

Db 263 LGTVLKMFLFYG 275

RESULT 8

US-10-975-692-2

; Sequence 2, Application US/10975692

; Publication No. US20060090221A1

; GENERAL INFORMATION:

; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

; APPLICANT: Browne, John A

; APPLICANT: Watts, James G

; APPLICANT: Wallis, Jennifer L.

; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF

; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS

; FILE REFERENCE: 4630-58963-02

; CURRENT FILING DATE: 2004-10-26

; PRIOR FILING DATE: 2004-10-26

; PRIOR APPLICATION NUMBER: US/10/975.693

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: PCT/US99/28655

; PRIOR FILING DATE: 1999-12-06

; PRIOR APPLICATION NUMBER: US 60/111,301

; PRIOR FILING DATE: 1998-12-07

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in version 3.3

; SEQ ID NO 2

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;  
Best Local Similarity 43.8%; Pred. No. 59;  
Matches 7; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17  
||:|:|:|:|:|:|  
Db 130 IRKLETFITLFAFY 145

## RESULT 9

US-10-505-928-543  
; Sequence 543, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 543  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;  
Best Local Similarity 47.1%; Pred. No. 70;  
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 3 RRFL--GSIWRFIRAFY 17  
||| |:|:|:|:|:|  
Db 473 RRFTQSGDLYHRKPH 489

## RESULT 10

US-11-169-140-109  
; Sequence 109, Application US/11169140  
; Publication No. US20060099150A1  
; GENERAL INFORMATION:  
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou, L.  
; APPLICANT: SHERIDAN, Philip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven  
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE  
; TITLE OF INVENTION: BARRIERS  
; FILE REFERENCE: 11474-037-999  
; CURRENT APPLICATION NUMBER: US/11/169,140  
; CURRENT FILING DATE: 2005-06-27  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/949,039  
; PRIOR FILING DATE: 2001-09-06  
; PRIOR APPLICATION NUMBER: 09/969,748  
; PRIOR FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 109  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Simian  
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;  
Best Local Similarity 42.1%; Pred. No. 35;  
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 GIRRFLGSIW----RPIR 14  
|:|:|:|:|:|:|  
Db 158 GIVLALGAVWCVARARPIR 176

## RESULT 11

US-11-204-427-7  
; Sequence 7, Application US/11204427  
; Publication No. US20060100146A1  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L  
; APPLICANT: Turkish, Aaron R  
; APPLICANT: Billheimer, Jeffrey T  
; APPLICANT: Cromley, Debra  
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES  
; FILE REFERENCE: 0575/72796/JPW/AJW/JCS  
; CURRENT APPLICATION NUMBER: US/11/204,427  
; CURRENT FILING DATE: 2005-08-15  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17  
:|:|:|:|:|:|  
Db 84 AIWRQLRDYY 93

## RESULT 12

US-11-304-129-40  
; Sequence 40, Application US/11304129  
; Publication No. US20060088915A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: TAKATSU, Yoshihiro  
; APPLICANT: WATANABE, Takuya  
; APPLICANT: TERAQ, Yasuko  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: HINUMA, Syuji  
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
; FILE REFERENCE: 2762US0P  
; CURRENT APPLICATION NUMBER: US/11/304,129  
; CURRENT FILING DATE: 2005-12-15  
; PRIOR APPLICATION NUMBER: US/10/333,192  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: JP 2000-217442  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: JP 2001-26779  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 40  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Rat  
US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;  
Best Local Similarity 46.2%; Pred. No. 75;



Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17

Db 216 FCGQIWPVDQQFY 228

RESULT 13

US-11-304-129-48  
; Sequence 48, Application US/11304129  
; Publication No. US2006008915A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: TAKATSU, Yoshihiro  
; APPLICANT: WATANABE, Takuya  
; APPLICANT: TERAOKA, Yasuko  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: HINUMA, Syuji  
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
; FILE REFERENCE: 2762USOP  
; CURRENT APPLICATION NUMBER: US/11/304,129  
; CURRENT FILING DATE: 2005-12-15  
; PRIOR APPLICATION NUMBER: US/10/333,192  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: JP 2000-217442  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: JP 2001-26779  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 48  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Mouse  
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;

Best Local Similarity 46.2%; Pred. No. 75;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17

Db 216 FCGQIWPVDQQFY 228

RESULT 14

US-10-505-928-545  
; Sequence 545, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 545  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;

Best Local Similarity 33.3%; Pred. No. 90;

Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 RFLGSIWRFIRAFY 18

| : | : |

Db 339 RYSSBYHYVGGFY 353

RESULT 15

US-10-505-928-853  
; Sequence 853, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 853  
; LENGTH: 1531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;

Best Local Similarity 50.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17

Db 1122 LGLIYFVQRFY 1133

Search completed: May 19, 2006, 15:28:18

Job time : 2.14286 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds  
(without alignments)

87.287 Million cell updates/sec

Title: US-10-712-447-13

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34231	Ado34231 Synthetic
2	98	100.0	18	ADO34225	Ado34225 Synthetic
3	98	100.0	18	ADO34228	Ado34228 Synthetic
4	98	100.0	18	ADO34236	Ado34236 Synthetic
5	98	100.0	18	ADO34233	Ado34233 Synthetic
6	95	95.9	18	ADO34314	Ado34314 Synthetic
7	94	95.9	18	ADO34354	Ado34354 Synthetic
8	94	95.9	18	ADO34338	Ado34338 Synthetic
9	94	95.9	18	ADO34352	Ado34352 Synthetic
10	94	95.9	18	ADO34340	Ado34340 Synthetic
11	94	95.9	18	ADO34339	Ado34339 Synthetic
12	92	93.9	18	ADO34297	Ado34297 Synthetic
13	92	93.9	18	ADO34244	Ado34244 Synthetic
14	92	93.9	18	ADO34276	Ado34276 Synthetic
15	90	91.8	18	ADO34227	Ado34227 Synthetic
16	90	91.8	18	ADO34350	Ado34350 Synthetic
17	89	90.8	18	ADO34322	Ado34322 Synthetic
18	88	89.8	18	ADO34336	Ado34336 Synthetic
19	88	89.8	18	ADO34335	Ado34335 Synthetic
20	88	89.8	18	ADO34337	Ado34337 Synthetic
21	88	89.8	18	ADO34241	Ado34241 Synthetic
22	87	88.8	18	ADO34240	Ado34240 Synthetic
23	86	87.8	18	ADO34284	Ado34284 Synthetic

24	86	87.8	18	8	ADO34305	Ado34305 Synthetic
25	85	86.7	18	8	ADO34239	Ado34239 Synthetic
26	85	86.7	18	8	ADO34344	Ado34344 Synthetic
27	85	86.7	18	8	ADO34319	Ado34319 Synthetic
28	84	85.7	18	8	ADO34245	Ado34245 Synthetic
29	84	85.7	18	8	ADO34301	Ado34301 Synthetic
30	84	85.7	18	8	ADO34343	Ado34343 Synthetic
31	84	85.7	18	8	ADO34318	Ado34318 Synthetic
32	82	83.7	18	8	ADO34302	Ado34302 Synthetic
33	82	83.7	18	8	ADO34279	Ado34279 Synthetic
34	82	83.7	18	8	ADO34303	Ado34303 Synthetic
35	82	83.7	18	8	ADO34242	Ado34242 Synthetic
36	82	83.7	18	8	ADO34300	Ado34300 Synthetic
37	82	83.7	18	8	ADO34281	Ado34281 Synthetic
38	82	83.7	18	8	ADO34317	Ado34317 Synthetic
39	81	82.7	18	8	ADO34323	Ado34323 Synthetic
40	81	82.7	18	8	ADO34280	Ado34280 Synthetic
41	80	81.6	18	8	ADO34264	Ado34264 Synthetic
42	79	80.6	18	8	ADO34320	Ado34320 Synthetic
43	78	79.6	18	2	AA118917	Aay18917 Lecithin:
44	78	79.6	18	2	AA119171	Aay19171 Lecithin:
45	78	79.6	18	2	AA119425	Aay19425 Lecithin:

#### ALIGNMENTS

##### RESULT 1

ID ADO34231 standard; peptide; 18 AA.

XX ADO34231;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 8.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;  
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
CC polypeptide. The invention further comprises an isolated nucleic acid  
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
CC a host cell, a recombinant cell or a transgenic, non-human subject  
CC (including animal or plant) comprising the synthetic apolipoprotein-E  
CC mimicking polypeptide encoding polynucleotide; a composition comprising  
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYG 18  
 |||||  
 DB 1 GIRRFGLSIWRFIRAFYG 18  
 |||||

RESULT 2  
 ADO34225  
 ID ADO34225 standard; peptide; 18 AA.  
 AC ADO34225;  
 XX  
 XX 12-AUG-2004 (first entry)  
 DT  
 DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.  
 DE  
 XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiatic;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 18 /note= "C-terminal amide"  
 FT  
 FT  
 FT  
 XX WO2004043403-A2.  
 PN  
 XX 27-MAY-2004.  
 PD  
 XX 13-NOV-2003; 2003WO-US036268.  
 PF  
 XX 13-NOV-2002; 2002US-0425821P.  
 PR  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Anantharamiah GM, Garber DW, Datta G;  
 PI WPI; 2004-411629/38.  
 DR  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 XX comprises an amino acid sequence.  
 XX  
 XX Claim 4; SEQ ID NO 2; 79pp; English.  
 PS  
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 XX polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYG 18  
 |||||  
 DB 1 GIRRFGLSIWRFIRAFYG 18  
 |||||

RESULT 3  
 ADO34228  
 ID ADO34228 standard; peptide; 18 AA.  
 XX  
 AC ADO34228;  
 XX  
 XX 12-AUG-2004 (first entry)  
 DT  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.  
 DE  
 XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiatic;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 XX Synthetic.  
 OS  
 XX WO2004043403-A2.  
 PN  
 XX 27-MAY-2004.  
 PD  
 XX 13-NOV-2003; 2003WO-US036268.  
 PF  
 XX 13-NOV-2002; 2002US-0425821P.  
 PR  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Anantharamiah GM, Garber DW, Datta G;  
 PI WPI; 2004-411629/38.  
 DR  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 XX comprises an amino acid sequence.  
 XX  
 XX Claim 4; SEQ ID NO 5; 79pp; English.  
 PS  
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 XX polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject

CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRIFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRIFIRAFYG 18

RESULT 4  
 ADO34236  
 ID ADO34236 standard; peptide; 18 AA.

AC ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRIFIRAFYG 18  
 |||||  
 Db 1 GIRRFLGSIWRIFIRAFYG 18

RESULT 5  
 ADO34233  
 ID ADO34233 standard; peptide; 18 AA.

AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic, and  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GIRRFGLSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFGLSIWRFIRAFYG 18  
 |||||  
 RESULT 6  
 ADO34314  
 ID ADO34314 standard; peptide; 18 AA.  
 XX  
 AC ADO34314;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2004043403-A2.  
 XX  
 XX 27-MAY-2004.  
 XX  
 XX 13-NOV-2003; 2003WO-US036268.  
 PF  
 XX 13-NOV-2002; 2002US-0425821P.  
 PR  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Anantharamiah GM, Garber DW, Datta G;  
 PI  
 XX WPI; 2004-411629/38.  
 DR  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 XX  
 XX Claim 4; SEQ ID NO 91; 79pp; English.  
 PS  
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic, and  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 96.9%; Score 95; DB 8; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GIRRFGLSIWRFIRAFYG 18  
 |||||  
 Db 1 GIRRFGLSIWRFIRAFYG 18  
 |||||  
 RESULT 7  
 ADO34354  
 ID ADO34354 standard; peptide; 18 AA.  
 XX  
 AC ADO34354;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.  
 XX  
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2004043403-A2.  
 XX  
 XX 27-MAY-2004.  
 XX  
 XX 13-NOV-2003; 2003WO-US036268.  
 PF  
 XX 13-NOV-2002; 2002US-0425821P.  
 PR  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Anantharamiah GM, Garber DW, Datta G;  
 PI  
 XX WPI; 2004-411629/38.  
 DR  
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.  
 XX  
 XX Claim 4; SEQ ID NO 131; 79pp; English.  
 PS  
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8  
 ADO34338  
 ID ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 115; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9  
 ADO34352  
 ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 129; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18  
 |||||:||||:||||  
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 10

ADO34340  
 ID ADO34340 standard; peptide; 18 AA.

XX ADO34340;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiand;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiand, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 11

ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiand;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiand, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is



The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector comprising the synthetic apolipoprotein-E mimicking polypeptide; a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipaseic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, and bird).

CC chimpanzee or orangutan); for treating coronary artery disease.  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYVG 18  
 |||||:|||||:|||||  
 Db 1 GIRRFGLSIWRFIRAFYVG 18

## RESULT 14

ADO34276  
 ID ADO34276 standard; peptide; 18 AA.

AC ADO34276;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1.18 /note= "All Lys residues are DiMethyl-Lysine"

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYVG 18  
 |||||:|||||:|||||  
 Db 1 GIRRFGLSIWRFIRAFYVG 18

## RESULT 15

ADO34227  
 ID ADO34227 standard; peptide; 18 AA.

AC ADO34227;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking related R18L linear peptide.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX

SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.1e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18

|||||

Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:30  
Job time : 95.2857 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds  
(without alignments)  
121.233 Million cell updates/sec

Title: US-10-712-447-13  
Perfect score: 98  
Sequence: 1 GIRRFGLSIWRFIRAFYG 18  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	S76462	hypothetical prote
2	45	45.9	178	A75578	transcription regu
3	44	44.9	461	G64537	2-oxoglutarate/mal
4	44	44.9	589	A34341	poly(3-hydroxybuty
5	44	44.9	806	A84060	leucyl-tRNA synthet
6	44	44.9	861	H64102	leucine-tRNA ligas
7	43.5	44.4	1025	AH3568	acriflavin resista
8	43	43.9	265	T32316	hypothetical prote
9	43	43.9	489	B84733	probable cytochrom
10	43	43.9	516	T33269	hypothetical prote
11	43	43.9	812	A46417	NIP1 protein - yea
12	43	43.9	1607	T04583	TMV resistance pro
13	42.5	43.4	407	T12085	reverse transcript
14	42.5	43.4	760	E84953	penicillin-binding
15	42	42.9	107	T52113	probable transcrip
16	42	42.9	214	D72540	hypothetical prote
17	42	42.9	228	T15530	hypothetical prote
18	42	42.9	237	B72692	hypothetical prote
19	42	42.9	246	I54412	MHC HLA-A cell sur
20	42	42.9	258	F71707	o-antigen export s
21	42	42.9	258	D97700	o-antigen export s
22	42	42.9	273	HLH069	MHC class I histoc
23	42	42.9	365	HLH042	MHC class I histoc
24	42	42.9	365	I38443	Gene HLA-A-0203 pr
25	42	42.9	365	I61902	MHC class I histoc
26	42	42.9	365	I37542	MHC class I histoc
27	42	42.9	365	I84448	MHC class I histoc
28	42	42.9	365	I61857	MHC HLA-A2.4a chai
29	42	42.9	365	I38442	gene HLA-A-0205 pr

30	42	42.9	537	2	T04745	hypothetical prote
31	42	42.9	803	2	AD1282	leucyl-tRNA synthet
32	42	42.9	803	2	AD1653	leucyl-tRNA synthet
33	42	42.9	804	2	B89961	leucyl-tRNA synthet
34	42	42.9	804	2	D69650	leucine-tRNA ligas
35	41.5	42.3	790	2	T50337	homolog to drosoph
36	41	41.8	131	2	AG2115	hypothetical prote
37	41	41.8	265	2	C21595	trifap protein - Esc
38	41	41.8	279	2	E64109	dimethylsulfoxide
39	41	41.8	359	2	T20575	hypothetical prote
40	41	41.8	364	2	AF2599	hypothetical prote
41	41	41.8	364	2	G97381	probable permease
42	41	41.8	384	2	T08940	hypothetical prote
43	41	41.8	406	2	F96571	hypothetical prote
44	41	41.8	503	2	D96776	hypothetical prote
45	41	41.8	519	1	T02263	cytochrome P450 DW

ALIGNMENTS

RESULT 1  
S76462  
hypothetical protein - Synchocystis sp. (strain PCC 6803)  
C:Species: Synchocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S76462  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76462  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-627 <KAN>  
A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID: A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;  
Best Local Similarity 38.9%; Pred. No. 8.1;  
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy	1	GIRRFGLSIWRFIRAFYG 18
Db	597	GLEQLLKKIWQLRQKFG 614

RESULT 2  
A75578  
transcription regulator, MarR family - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: A75578  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: A75578  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-178 <WHI>  
A:Cross-references: UNIPROT:Q9RYR0; UNIPARC:UPI00000D3BE4; GB:AE001863; GB:AE001825; NID: A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRA0248  
A:Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14  
| | | | |  
Db 23 ILRFLGSIWRLNR 35

RESULT 3  
G64537  
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: G64537  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:9739467; PMID:9252185  
A:Accession: G64537  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-461 <TOM>  
A:Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143  
C:Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14  
: | | | | |  
Db 297 VRLLSFWRFVR 309

RESULT 4  
A34341  
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus  
C:Species: Alcaligenes eutrophus  
C>Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: A34341; A39190  
R:Peoples, O.P.; Sinskey, A.J.  
J. Biol. Chem. 264, 15298-15303, 1989  
A:Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident  
A:Reference number: A34341; MUID:89359357; PMID:2670936  
A:Accession: A34341  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-589 <PEO>  
A:Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:  
R:Schubert, P.; Krueger, N.; Steinbuechel, A.  
J. Bacteriol. 173, 168-175, 1991  
A:Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt  
omoter.  
A:Reference number: A39190; MUID:91100279; PMID:1987116  
A:Accession: A39190  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-219 <SCH>  
A:Cross-references: UNIPARC:UPI0000165162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:  
A>Note: the authors translated the codon TAC for residue 120 as Thr  
C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc  
C:Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;  
Best Local Similarity 47.8%; Pred. No. 33;  
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RREFLGSIW-----RTRAFY 17  
| | | | |

Db 100 RRFAGDAWETNLPYRFAAAFY 120

RESULT 5  
A84060  
leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: A84060  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: A84060  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-806 <STO>  
A:Cross-references: UNIPROT:Q9K788; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: leuS  
C:Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;  
Best Local Similarity 53.8%; Pred. No. 45;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13  
| | | | |  
Db 622 GARRFLDRVWRL 634

RESULT 6  
H64102  
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)  
N:Alternate names: leucyl-tRNA synthetase  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: H64102  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: H64102  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-861 <TIGR>  
A:Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:142023; NID:g15:  
C:Genetics:  
A:Gene: leuS  
C:Superfamily: leucine-tRNA ligase  
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;  
Best Local Similarity 46.2%; Pred. No. 48;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13  
| | | | |  
Db 665 GAKRFLGRVWNLV 677

RESULT 7  
AH3568  
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:Accession: AH3568  
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.  
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc



## C;Genetics:

A;Gene: SGD:NIP1  
A;Cross-references: SGD:S0004926; MIPS:YMR309C  
A;Map position: 13R

Query Match 43.9%; Score 43; DB 2; Length 812;  
Best Local Similarity 53.8%; Pred. No. 66;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFI 13

|::| ||||: |:

Db 361 GVKRLGISFV 373

## RESULT 12

T04583

TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C;Accession: T04583; T05507

R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duysterhoeft, A.; Jessee, T. submitted to the Protein Sequence Database, March 1998

A;Reference number: Z15378

A;Accession: T04583

A;Molecule type: DNA

A;Residues: 1-1607 &lt;BEV&gt;

A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141

A;Experimental source: cultivar Columbia; BAC clone F23E13

R;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelke submitted to the Protein Sequence Database, April 1998

A;Reference number: Z15418

A;Accession: T05507

A;Molecule type: DNA

A;Residues: 1448-1607 &lt;BE2&gt;

A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373

A;Experimental source: cultivar Columbia; BAC clone T19K4

C;Genetics:

A;Map position: 4

A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3

A;Note: F23E13.30; T19K4.270

Query Match 43.9%; Score 43; DB 2; Length 1607;

Best Local Similarity 72.7%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16

||| ||||

Db 1321 LGSSWRLRGF 1331

## RESULT 13

T12085

reverse transcriptase homolog - fava bean (fragment)

C;Species: Vicia faba (fava bean)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T12085

R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.

submitted to the EMBL Data Library, September 1997

A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.

A;Reference number: Z17406

A;Accession: T12085

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-407 &lt;KIN&gt;

A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000AAD3D; EMBL:AB007466; NID:d1170509;

A;Experimental source: guard cell protoplasts

C;Superfamily: pol polyprotein

Query Match

Best Local Similarity 43.4%; Score 42.5; DB 2; Length 407;

Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GRRFLGSIW--RFIRAF 16

Db 178 GRRFLGHVGFRRFIRDF 196

||| |||: |||||

## RESULT 14

E84953

penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002

C;Accession: E84953

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: E84953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-760 &lt;STO&gt;

A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mrcB; BU200

C;Superfamily: penicillin-binding protein 1B

Query Match 43.4%; Score 42.5; DB 2; Length 760;

Best Local Similarity 44.4%; Pred. No. 74;

Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFLGSIWRFIRAFYG 18

|||: ||||: ||

Db 32 INRFINGKWNPTSIYG 49

## RESULT 15

T52113

probable transcription co-activator KIWI [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C;Accession: T52113

R;Cornack, R.S.; Hahlbrock, K.; Somssich, I.E.

Plant J. 14, 685-92, 1998

A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hy

A;Reference number: Z25848; MUID:98346011; PMID:9681033

A;Accession: T52113

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-107 &lt;COR&gt;

A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.1

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: KIWI

A;Map position: V

C;Function:

A;Description: probably plays a role in gene activation during pathogen defence and plant

C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match 42.9%; Score 42; DB 2; Length 107;

Best Local Similarity 50.0%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17

:|: |||||

Db 54 VRNNGKIWDIREFY 69

Search completed: May 19, 2006, 14:39:56

Job time : 18.2857 secs



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds  
(without alignments)  
144.247 Million cell updates/sec

Title: US-10-712-447-13  
Perfect score: 98  
Sequence: 1 GIRRFLGSIWRFI AFYV 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	Q3APV5_CHLCH	Q3apv5 chlorobium
2	54	55.1	670	Q25271_LEPDE	Q25271 leptinotars
3	52	53.1	735	Q9F7V7_RHILV	Q9f7v7 rhizobium 1
4	52	53.1	805	Q44QD1_CHILLI	Q44qdi chlorobium
5	52	53.1	816	Q43K01_CHLHB	Q43k01 chlorobium
6	51	52.0	407	Q39L57_BURK3	Q39l57 burkholderi
7	51	52.0	408	Q456F4_BURK	Q456f4 burkholderi
8	51	52.0	408	Q4LK44_BURK	Q4lk44 burkholderi
9	50	51.0	579	1_XKR7_HUMAN	Q5gh72 homo sapien
10	50	51.0	579	1_XKR7_PANTR	Q49l81 pan troglod
11	50	51.0	580	1_XKR7_MOUSE	Q5gh64 mus musculus
12	50	51.0	580	1_XKR7_RAT	Q5gh56 rattus norv
13	49	50.0	409	Q4BFM2_BURVI	Q4bfm2 burkholderi
14	49	50.0	449	Q3PK79_PARDE	Q3pk79 paracoccus
15	49	50.0	488	Q84ZW1_PEA	Q84zw1 pisum sativ
16	48	49.0	188	Q2ILN7_DELT	Q2iln7 anaeromyxob
17	48	49.0	288	Q8R587_MOUSE	Q8r587 mus musculus
18	48	49.0	435	Q2JIT0_9CYAN	Q2jit0 cyanobacter
19	48	49.0	578	1_XKR6_TETNG	Q49l88 tetradodon n
20	48	49.0	578	Q5GH49_FUGRU	Q5gh49 fugu rubrip
21	48	49.0	627	Q54A89_SYNY3	P74489 synecocyst
22	47.5	48.5	240	Q97035_HAESO	P97035 haemophilus
23	47.5	48.5	577	Q36XB4_RHOPA	Q36xb4 rhodospseudo
24	47.5	48.5	577	Q37C12_RHOPA	Q37cl2 rhodospseudo
25	47.5	48.5	807	Q3VMG0_9CHLB	Q3vmg0 pelodictyon
26	47	48.0	486	Q5U414_XENLA	Q5u414 xenopus lae
27	47	48.0	487	Q32N49_XENLA	Q32n49 xenopus lae
28	47	48.0	910	Q3ZDS6_ORYZA	Q5zds6 oryza sativ
29	46	46.9	361	Q2NUB5_SODGL	Q2nub5 sodalis glo
30	46	46.9	385	Q5ZPA2_9DELT	Q5zpa2 angiococcus
31	46	46.9	540	Q5GH65_MOUSE	Q5gh65 mus musculus

RESULT 1  
Q3APV5\_CHLCH  
ID Q3APV5\_CHLCH PRELIMINARY; PRT; 805 AA.  
AC Q3APV5\_ CHLCH  
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.  
DT 21-FEB-2006, sequence version 1.  
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).  
GN OrderedLocusNames=Cag\_1688;  
OS Chlorobium chlorochromatii (strain Cad3).  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium/Felodictyon group; Chlorobium.  
OX NCBI\_TaxID=340177;  
RN [1]  
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RG US DOE Joint Genome Institute;  
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,  
RA Hammon N., Israni S., Pittluck S., Bryant D., Schmutz J., Larimer F.,  
RA Land M., Kyrpides N., Ivanova N., Richardson P.;  
RA "Complete sequence of Chlorobium chlorochromatii Cad3.";  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC EMBL; CP000108; ABB28940.1; -; Genomic\_DNA.  
DR GO; GO:000524; P:ATP binding; IEA.  
DR GO; GO:0004823; P:leucine-tRNA ligase activity; IEA.  
DR GO; GO:0016874; P:ligase activity; IEA.  
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.  
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.  
SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;  
Best Local Similarity 69.2%; Pred.No. 3.2; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 2;

Qy 1 GIRRFLGSIWRFI 13  
||| :||| :||| :  
Db 622 GISRFLECKVRFV 634

RESULT 2  
Q25271\_LEPDE  
ID Q25271\_LEPDE PRELIMINARY; PRT; 670 AA.  
AC Q25271\_  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DE Diapause protein 1 (Fragment).  
DE Diapause protein 1 (Fragment).  
GN Name=Dp19;  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

```

OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
OC Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RP de Kort C.A.D., Koopmanschap A.B.;
RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding
RT diapause protein 1, an amylophorin-type storage hexamer of the Colorado
RT potato beetle.";
RL J. Insect Physiol. 40:527-535(1994).
CC -----
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CC -----
DR EMBL; X76080; CAA53691.1; -; mRNA.
DR HSP; P04253; ILL1.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0008986; Hemocyanin.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR005203; Hemocyanin_C.
DR InterPro; IPR005204; Hemocyanin_N.
DR PANTHER; PTHR11511; Hemocyanin; 1.
DR Pfam; PF03723; Hemocyanin_C; 1.
DR Pfam; PF03722; Hemocyanin_M; 1.
DR Pfam; PF03722; Hemocyanin_N; 1.
DR PRINTS; PR00187; HAEMOCYANIN.
DR PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;

Query Match 55.1%; Score 54; DB 2; Length 670;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRFGLSGIWRIFAFY 18
DB 351 RKFGALMSYLRHFFG 366

RESULT 3
Q9FV7V_RHLV
ID Q9FV7V_RHLV PRELIMINARY; PRT; 735 AA.
AC Q9FV7V
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE ABC transporter RzcB.
GN NamesrzcB;
OS Rhizobium leguminosarum bv. viciae.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=305;
RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
RT "Analysis of the genetic region encoding a novel rhizobiocin from
RT Rhizobium leguminosarum bv. viciae strain 305.";
RL Can. J. Microbiol. 47:495-502(2001).
CC -----
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CC -----
DR EMBL; AF273216; AAG25076.1; -; Genomic_DNA.
DR HSP; P08716; IMT0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.

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DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_TM_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR005074; Peptidase_C39.
DR InterPro; PTHR10132; Type_I_sec_HlyB.
DR PANTHER; PTHR19242:SF74; Type_I_sec_HlyB; 1.
DR Pfam; PF00664; ABC membrane; 1.
DR Pfam; PF00005; ABC tran; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01846; type_I_sec_HlyB; 1.
DR PROSITE; PS50929; ABC_TMIF; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PS50990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;
Best Local Similarity 52.5%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRIFRAF 16
DB 161 GRRFLPAIWRVRAF 176

RESULT 4
Q44QD1_CHLLI
ID Q44QD1_CHLLI PRELIMINARY; PRT; 805 AA.
AC Q44QD1
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=ClimDRAFT_1980;
OS Chlorobium limicola DSM 245.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290315;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Chlorobium limicola
RT DSM 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium limicola DSM
RT 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAJ0100009; EAA43320.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNAsyn_1a.
DR Pfam; PF00133; tRNA-synt_1; 1.

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DR PRINTS; PRO0985; TRNASYNTHLEU.
KW Aminoacyl-tRNA synthetase_bact; 1.
SQ SEQUENCE 805 AA; 91997 MW; D4P3FE28F9E92DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFI 13
||| :||| :
Db 622 GISRFLGKVRWLV 634

RESULT 5
O43K01_9CHLB
ID O43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC O43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
DR EMBL; AAI01000002; EAM35935.1; -; Genomic_DNA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNA_synth_1a.
DR Pfam; PF00133; tRNA-synt_1_1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFI 13
||| :||| :
Db 622 GISRFLGKVRWLV 634

RESULT 6
Q39L57_BURS3
ID Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
AC Q39L57;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocuNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RA "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; CP000151; ABB06809.1; -; Genomic_DNA.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFI 17
||| :||| :
Db 327 GIRQMLGHVQWTRSSY 343

RESULT 7
Q456F4_9BURK
ID Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=BcendRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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```

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CC -----
DR EMBL; AAH01000010; EAM12352.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;

Query Match      52.0%; Score 51; DB 2; Length 408;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFY 17
Db 328 GIRQMLGHVWQWTRSSY 344
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RESULT 8
Q4LK44_9BURK PRELIMINARY; PRT; 408 AA.
AC Q4LK44;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DE 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_1071;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=331272;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Piclucck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAH01000063; EAM16412.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;

Query Match      52.0%; Score 51; DB 2; Length 408;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFY 17
Db 328 GIRQMLGHVWQWTRSSY 344
||||:|:|:|:|:|

RESULT 9
XKR7_HUMAN STANDARD; PRT; 579 AA.
ID XKR7_HUMAN
AC QSGH72; Q9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.

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GN Name=XKR7; Synonyms=C20orf159, XRG7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP Huang C.-H., Chen Y.;
RA "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Corby N.R.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.B., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaibo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McElay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; AY534245; AA07094.1; -; mRNA.
DR EMBL; AL031658; CAB8102.1; ALT SEQ; Genomic_DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
DR HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
FT CHAIN 1 579 XK-related protein 7.
FT /FTID=PRO_0000190788.
FT TRANSMEM 59 79 Potential.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 314 334 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
FT SEQUENCE 579 AA; 63826 MW; D8D0FF64B9ED53D CRC64;

Query Match      51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSIRWFIRAFY 17
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Db      190 LGQVWRYLRALY 201

RESULT 10
ID_     XKR7 PANTR      STANDARD;      PRT;      579 AA.
AC      Q49LS1;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      13-SEP-2005, sequence version 1.
DT      07-FEB-2006, entry version 6.
DE      XK-related protein 7.
GN      Name=XKR7; Synonyms=XRG7;
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC      Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      -----
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CC      -----
DR      EMBL; AY702910; AAV83783.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      579
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      314     334
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      579 AA; 63593 MW; 6DFE11903B85D4 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 LGSWRFIRAFY 17
      |||:|:|:|
Db      190 LGQVWRYLRALY 201

RESULT 11
ID_     XKR7 MOUSE      STANDARD;      PRT;      580 AA.
AC      Q5GH64;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 10.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      -----
DR      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
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CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      -----
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CC      -----
DR      EMBL; AY534253; AAT07102.1; -; mRNA.
DR      Ensembl; ENSMUSG0000042631; Mus musculus.
DR      MGI; MGI:3526711; Xkr7.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 LGSWRFIRAFY 17
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Db      190 LGQVWRYLRALY 201

RESULT 12
ID_     XKR7 RAT          STANDARD;      PRT;      580 AA.
AC      Q5GH56;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 8.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      -----
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CC      -----
DR      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
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[illegible]

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RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";
RL Plant Physiol. 131:335-344(2003).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL; AF537321; AAC23063.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR02401; EP450I.
DR PANTHER; PTHR19383; Cytochrome_P450; 1.
DR Pfam; PF00067; P450; 2.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred. No. 50;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5.FLGSINRPIRAF 16
|:|:| |:|
Db 54.FIGNWISFLRAF 65

Search completed: May 19, 2006, 14:38:12
Job time : 124.429 secs
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Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFYG 18  
||:|||||:|:|:|  
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 2  
US-08-940-093-242  
; Sequence 242, Application US/08940093  
; Patent No. 6037323  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,093  
; FILING DATE: 29-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0006-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6037323e  
; US-08-940-093-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFYG 18  
||:|||||:|:|:|  
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 3  
US-08-940-096-242  
; Sequence 242, Application US/08940096  
; Patent No. 6046166  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811

APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,096  
FILING DATE: 29-SEP-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6046166e  
US-08-940-096-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFYG 18  
||:|||||:|:|:|  
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 4  
US-09-465-719-242  
; Sequence 242, Application US/09465719  
; Patent No. 6265377  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRIFAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-NOV-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

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;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRIFAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
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STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,833  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6602854e  
US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
||:|||||:|:|  
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 10  
US-09-453-826-242  
Sequence 242, Application US/09453826  
Patent No. 6630450  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,826  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6630450e  
US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;  
Best Local Similarity 72.2%; Pred. No. 1.1e-05;  
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18  
||:|||||:|:|  
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 11  
US-09-453-840-242  
Sequence 242, Application US/09453840  
Patent No. 6716816  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,840  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFVG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFVG 18
Db 1 GIKKFLGSIWKFIRAFVG 18
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```
RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFVG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

;; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

;; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFFIRAFVG 18

Db 1 GIKKFLGSIWKFKAFVG 18

RESULT 15

US-09-465-718-242

;; Sequence 242, Application US/09465718

;; Patent No. 6900177

;; GENERAL INFORMATION:

;; APPLICANT: Dasseux, Jean-Louis

;; APPLICANT: Sekul, Renate

;; APPLICANT: Buttner, Klaus

;; APPLICANT: Cornut, Isabelle

;; APPLICANT: Metz, Gunther

;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

;; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

;; NUMBER OF SEQUENCES: 258

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718

;; FILING DATE: 17-Dec-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/940,096

;; FILING DATE: 29-SEP-1997

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

;; US-09-465-718-242

Query Match

Best Local Similarity 72.2%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFFIRAFVG 18

Db 1 GIKKFLGSIWKFKAFVG 18

Search completed: May 19, 2006, 14:42:54

Job time : 25.8571 secs

**This Page Blank (uspto)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds  
(without alignments)  
102.575 Million cell updates/sec

Title: US-10-712-447-13

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-98
18	88	89.8	18	4	US-10-712-447-112
19	88	89.8	18	4	US-10-712-447-113
20	88	89.8	18	4	US-10-712-447-114
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28	84	85.7	18	4	US-10-712-447-22	Sequence 22, Appl
29	84	85.7	18	4	US-10-712-447-78	Sequence 78, Appl
30	84	85.7	18	4	US-10-712-447-95	Sequence 95, Appl
31	84	85.7	18	4	US-10-712-447-120	Sequence 120, Appl
32	82	83.7	18	4	US-10-712-447-19	Sequence 19, Appl
33	82	83.7	18	4	US-10-712-447-56	Sequence 56, Appl
34	82	83.7	18	4	US-10-712-447-58	Sequence 58, Appl
35	82	83.7	18	4	US-10-712-447-77	Sequence 77, Appl
36	82	83.7	18	4	US-10-712-447-79	Sequence 80, Appl
37	82	83.7	18	4	US-10-712-447-80	Sequence 94, Appl
38	82	83.7	18	4	US-10-712-447-94	Sequence 97, Appl
39	81	82.7	18	4	US-10-712-447-57	Sequence 57, Appl
40	81	82.7	18	4	US-10-712-447-100	Sequence 100, Appl
41	80	81.6	18	4	US-10-712-447-41	Sequence 41, Appl
42	79	80.6	18	4	US-10-712-447-97	Sequence 242, Appl
43	78	79.6	18	3	US-09-865-989-242	Sequence 242, Appl
44	78	79.6	18	3	US-09-865-989-242	Sequence 242, Appl
45	78	79.6	18	4	US-10-099-574A-242	Sequence 242, Appl

#### ALIGNMENTS

RESULT 1  
US-10-712-447-2  
; Sequence 2, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: c-term amidated  
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18  
|||||  
Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 2  
US-10-712-447-5  
; Sequence 5, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13

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; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-91

Query Match          96.9%; Score 95; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||:|||||
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 7
US-10-712-447-115
; Sequence 115, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-115

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||:|||||
Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 8
US-10-712-447-116
; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 116
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||:|||||
Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 9
US-10-712-447-117
; Sequence 117, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-117

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||:|||||
Db 1 GRRFIGSIWRFIRAFYG 18

RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-129
```

```

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0;

QY      1 GIRRFLGSIWRFIRAFYG 18
          |||||:||||:||||
DB      1 GIRRFLGSIWRFIRAFYG 18

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131

```

```

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0;

QY      1  GRRFLGSIWRRFIRAFYG 18
          |:|||||:|||||
Db       1  GLRRFLGSIWRRFIRAFYG 18

RESULT 12
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-1230US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-21

```

Query Match	93.9%;	Score 92;	DB 4;	Length 18;
. Best Local Similarity	88.9%;	Pred. No. 7.9e-07;		

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Query Match          93.9%;      Score 92;      DB 4;      Length 18;
Best Local Similarity 88.9%;      Pred. NO. 7.9e-07;
Matches 16;      Conservative 2;      Mismatches 0;      Indels 0;      Caps 0;

QY      1      GIRRFLGSIWRFFIRAFYG 18
      ||:|||||
Db      1      GIKRFLGSIWRFFIKAFYG 18

RESULT 14
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

```
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GIRRFLGSIWRFIRAFYG 18
      |||||
Db      1 GIRRFLGSIWRFIRAFYG 18
      |||||

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4
Query Match      91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GIRRFLGSIWRFIRAFYG 18
      |||||
Db      1 GIRRFLGSIWRFIRAFYG 18
      |||||

Search completed: May 19, 2006, 15:27:56
Job time : 81.2857 secs
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; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
; FILE REFERENCE: MPI2001-288P1RCP10NMIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-242-505A-18

Query Match 37.8%; Score 37; DB 7; Length 403;  
Best Local Similarity 55.6%; Pred. No. 16;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRRFLGSIW 10  
: || ||| :  
Db 155 VRRVLGAV 163

RESULT 3  
US-09-949-925-142  
; Sequence 142, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 142  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (60)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-949-925-142

Query Match 37.2%; Score 36.5; DB 1; Length 60;  
Best Local Similarity 57.1%; Pred. No. 2.2;  
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
QY 5 FLGSIWRFIRAFYG 18  
: || : ||| :  
Db 31 FLILWIFV-AFYG 43

RESULT 4  
US-09-949-925-111  
; Sequence 111, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (74)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-949-925-111

Query Match 36.7%; Score 36; DB 1; Length 74;  
Best Local Similarity 54.5%; Pred. No. 3.3;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRF 12  
: || ||| :  
Db 59 LREVSGLIWRP 69

RESULT 5  
US-11-302-678-5  
; Sequence 5, Application US/11302678  
; Publication No. US20060088881A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012PIRNM\_OMNI  
US-11-302-678-5



; CURRENT APPLICATION NUMBER: US/11/302,678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-302-678-5

Query Match 36.7%; Score 36; DB 7; Length 599;  
Best Local Similarity 71.4%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LGSWRF 12  
Db 64 LGNVWF 70

RESULT 6  
US-11-242-505A-48  
; Sequence 48, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
; FILE REFERENCE: MPI2001-288RCPIONMIN  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;  
Best Local Similarity 50.0%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 0; Indels 5; Gaps 0;

Qy 6 LGSWRF 17

Db 195 LEEAWFLDAFY 206

RESULT 7  
US-10-511-937-2540  
; Sequence 2540, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlseuth, Jay  
; APPLICANT: Fry, Kirk, Robert  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2540  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2540

Query Match 34.7%; Score 34; DB 6; Length 351;  
Best Local Similarity 46.2%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 18  
Db 263 LGTVLWMLFYG 275

RESULT 8  
US-10-975-692-2  
; Sequence 2, Application US/10975692  
; Publication No. US20060090221A1  
; GENERAL INFORMATION:  
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION  
; APPLICANT: Browne, John A  
; APPLICANT: Wallis, James G  
; APPLICANT: Watts, Jennifer L.  
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS  
; FILE REFERENCE: 4630-58963-02  
; CURRENT APPLICATION NUMBER: US/10/975,692  
; CURRENT FILING DATE: 2004-10-26  
; PRIOR APPLICATION NUMBER: US 09/857,583  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/28655  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/111,301  
; PRIOR FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 447  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-975-692-2

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RESULT 10
US-11-169-140-109
; Sequence 109, Application US/11169140
; Publication No. US2006009150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANS-
; FILE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US 11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Simian
US-11-169-140-109

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Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17

Db 216 FCGQIWPVDQQFY 228

## RESULT 13

US-11-304-129-48  
; Sequence 48, Application US/11304129  
; Publication No. US2006008915A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTAKI, Tetsuya  
; APPLICANT: MASUDA, Yasushi  
; APPLICANT: TAKATSU, Yoshihiro  
; APPLICANT: WATANABE, Takuya  
; APPLICANT: TERAOKA, Yasuko  
; APPLICANT: SHINTANI, Yasushi  
; APPLICANT: HINUMA, Syuji  
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
; FILE REFERENCE: 2762USOP  
; CURRENT APPLICATION NUMBER: US/11/304,129  
; CURRENT FILING DATE: 2005-12-15  
; PRIOR APPLICATION NUMBER: US/10/333,192  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: JP 2000-217442  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: JP 2001-26779  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 48  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Mouse  
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;  
Best Local Similarity 46.2%; Pred. No. 75;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17

Db 216 FCGQIWPVDQQFY 228

## RESULT 14

US-10-505-928-545  
; Sequence 545, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 545  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;  
Best Local Similarity 33.3%; Pred. No. 90;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 RFLGSIWRFIRAFY 18

| : : : |||

Db 339 RYYSSEYHYVGFY 353

## RESULT 15

US-10-505-928-853  
; Sequence 853, Application US/10505928  
; Publication No. US20060088532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 853  
; LENGTH: 1531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;  
Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17

Db 1122 LGLIYFFVQRFY 1133

Search completed: May 19, 2006, 15:28:17  
Job time : 3.14286 secs

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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds

(without alignments)  
87.287 Million cell updates/sec

Title: US-10-712-447-115

Perfect score: 98

Sequence: 1 GLRRFGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	98	100.0	18	8	ADO34338	Ado34338 Synthetic
2	98	100.0	18	8	ADO34339	Ado34339 Synthetic
3	94	95.9	18	8	ADO34231	Ado34231 Synthetic
4	94	95.9	18	8	ADO34354	Ado34354 Synthetic
5	94	95.9	18	8	ADO34225	Ado34225 Synthetic
6	94	95.9	18	8	ADO34228	Ado34228 Synthetic
7	94	95.9	18	8	ADO34236	Ado34236 Synthetic
8	94	95.9	18	8	ADO34340	Ado34340 Synthetic
9	94	95.9	18	8	ADO34233	Ado34233 Synthetic
10	94	95.9	18	8	ADO34350	Ado34350 Synthetic
11	91	92.9	18	8	ADO34314	Ado34314 Synthetic
12	90	91.8	18	8	ADO34352	Ado34352 Synthetic
13	88	89.8	18	8	ADO34297	Ado34297 Synthetic
14	88	89.8	18	8	ADO34244	Ado34244 Synthetic
15	88	89.8	18	8	ADO34276	Ado34276 Synthetic
16	86	87.8	18	8	ADO34227	Ado34227 Synthetic
17	86	87.8	18	8	ADO34335	Ado34335 Synthetic
18	85	86.7	18	8	ADO34322	Ado34322 Synthetic
19	84	85.7	18	8	ADO34336	Ado34336 Synthetic
20	84	85.7	18	8	ADO34337	Ado34337 Synthetic
21	84	85.7	18	8	ADO34241	Ado34241 Synthetic
22	83	84.7	18	8	ADO34240	Ado34240 Synthetic
23	83	84.7	18	8	ADO34344	Ado34344 Synthetic

24	82	83.7	18	8	ADO34284	Ado34284 Synthetic
25	82	83.7	18	8	ADO34305	Ado34305 Synthetic
26	81	82.7	18	8	ADO34239	Ado34239 Synthetic
27	81	82.7	18	8	ADO34319	Ado34319 Synthetic
28	80	81.6	18	8	ADO34245	Ado34245 Synthetic
29	80	81.6	18	8	ADO34301	Ado34301 Synthetic
30	80	81.6	18	8	ADO34343	Ado34343 Synthetic
31	80	81.6	18	8	ADO34318	Ado34318 Synthetic
32	78	79.6	18	8	ADO34302	Ado34302 Synthetic
33	78	79.6	18	8	ADO34279	Ado34279 Synthetic
34	78	79.6	18	8	ADO34303	Ado34303 Synthetic
35	78	79.6	18	8	ADO34242	Ado34242 Synthetic
36	78	79.6	18	8	ADO34300	Ado34300 Synthetic
37	78	79.6	18	8	ADO34281	Ado34281 Synthetic
38	78	79.6	18	8	ADO34317	Ado34317 Synthetic
39	77	78.6	18	8	ADO34323	Ado34323 Synthetic
40	77	78.6	18	8	ADO34280	Ado34280 Synthetic
41	76	77.6	18	8	ADO34264	Ado34264 Synthetic
42	76	77.6	18	8	ADO34342	Ado34342 Synthetic
43	75	76.5	18	8	ADO34320	Ado34320 Synthetic
44	74	75.5	18	2	AAV18917	AAV18917 Lecithin:
45	74	75.5	18	2	AAV19171	AAV19171 Lecithin:

#### ALIGNMENTS

##### RESULT 1

ADO34338 ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.

XX KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 115; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC myocardial infarction or atherosclerosis; and for reducing the risk of  
 CC also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFFIRAFYG 18  
 |||||  
 Db 1 GLRRFIGSIWRFFIRAFYG 18

# RESULT 2

ADO34339  
 ID ADO34339 standard; peptide; 18 AA.

XX AC ADO34339;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 116.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 116; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC myocardial infarction or atherosclerosis; and for reducing the risk of  
 CC also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFFIRAFYG 18  
 |||||  
 Db 1 GLRRFIGSIWRFFIRAFYG 18

# RESULT 3

ADO34231  
 ID ADO34231 standard; peptide; 18 AA.

XX AC ADO34231;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 8.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 8; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,







CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for breaking the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18

Db 1 GIRRFGLSIWRFIRAFYG 18

RESULT 8

ADO34340

ID ADO34340 standard; peptide; 18 AA.

AC ADO34340;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

PN WO2004043403-A2.

XX 27-MAY-2004.

PF 13-NOV-2003; 2003WO-US036268.

PR 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

PI Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for breaking the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18

Db 1 GIRRFGLSIWRFIRAFYG 18

RESULT 9

ADO34233

ID ADO34233 standard; peptide; 18 AA.

AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

PN WO2004043403-A2.

XX 27-MAY-2004.

PF 13-NOV-2003; 2003WO-US036268.

PR 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

PI Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,





The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is



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Query Match	48.0%;	Score 47;	DB 2;	Length 516;
Best Local Similarity	52.9%;	Pred. No. 9.8;		





Nature 357, 326-329, 1992  
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
A;Reference number: I37120; MUID:92289955; PMID:1317015  
A;Accession: S77965  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-365 <BBL>  
A;Cross-references: UNIPARC:UPI0000124E24; EMBL:MB43779; NID:G403143; PIDN:AAA59606.1; PII  
A;Experimental source: cell line GRC 138; isolate A\*0201  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992  
R;Castano, A.R.; Lopez de Castro, J.A.  
Immunogenetics 35, 344-346, 1992  
A;Title: Structure of the HLA-A \*0211 (A2.5) subtype: further evidence for selection-driven  
A;Reference number: S23593; MUID:92218010; PMID:1559719  
A;Accession: S23593  
A;Molecule type: protein  
A;Residues: 9-96, 'ID', 99-365 <CAS2>  
A;Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:G32156; PIDN:CAB56609.1; PII  
A;Note: this allele is designated A\*0211 (previously HLA-A2.5)  
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.  
Proc. Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979  
A;Title: Comparison of amino acid sequences of two human histocompatibility antigens, HL  
A;Reference number: A93834; MUID:80056745; PMID:92029  
A;Accession: A93834  
A;Molecule type: protein  
A;Residues: 25-55, 'Z', 57-60, 'B', 62, 'B', 64-66, 'Z', 68-74, 'X', 76-85, 'RXXX', 90-94, 'AH', 97, 'V'  
A;Cross-references: UNIPARC:UPI00001737EE  
A;Note: this sequence has been revised in reference A93919  
R;Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.  
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982  
A;Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA-A2  
A;Reference number: A93919; MUID:82247941; PMID:6179086  
A;Accession: A93919  
A;Molecule type: protein  
A;Residues: 25-85, 'RXXX', 90-94, 'AH', 97, 'V', 99-112, 'Z', 114-118, 'LZ', 121-125, 'X', 127-131, '  
'232-265, 'E', 267-294 <LOP>  
A;Cross-references: UNIPARC:UPI00001737EF  
R;Silver, M.L.; Parker, K.C.; Wiley, D.C.  
Nature 350, 619-622, 1991  
A;Title: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-mic  
A;Reference number: S14802; MUID:91204056; PMID:2017257  
A;Accession: S14802  
A;Molecule type: protein  
A;Residues: 25-36 <SLI>  
A;Cross-references: UNIPARC:UPI000001737F0  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: 6p21.3-6p21.3  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status expe  
F;25-114/Domain: alpha-1 <EX1>  
F;115-206/Domain: alpha-2 <EX2>  
F;220-285/Domain: immunoglobulin homology <IMM>  
F;307-331/Domain: transmembrane #status predicted <TM>  
F;332-365/Domain: intracellular #status predicted <INT>  
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;125-188,227-283/Disulfide bonds: #status predicted

Query Match 44.9%; Score 44; DB 1; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 6 IGSWRFIRAFY 17  
DB 127 VGSDWRFRLRGYH 138  
RESULT 7  
138443

gene HLA-A-0203 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
A;Reference number: I37120; MUID:92289955; PMID:1317015  
A;Accession: I38443  
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.  
J. Immunol. 139, 936-941, 1987  
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28  
A;Reference number: I38441; MUID:87252273; PMID:3496393  
A;Accession: I38443  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016A05E; EMBL:U03863; NID:G432438; PIDN:AAA03604.1; PII  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>  
Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 6 IGSWRFIRAFY 17  
DB 127 VGSDWRFRLRGYH 138  
RESULT 8  
161902  
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A\*021  
C;Species: Homo sapiens (man)  
A;Variety: isolate A\*0212  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 23-Jul-1999  
C;Accession: I61902  
R;Balich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I  
Nature 357, 326-329, 1992  
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
A;Reference number: I37120; MUID:92289955; PMID:1317015  
A;Accession: I61902  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AD39; db:MB4378; NID:G187625; PIDN:AAA59604.1; PII:G  
A;Experimental source: cell line KRC 033; isolate A\*0212  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: 6p21.3-6p21.3  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predic  
F;220-285/Domain: immunoglobulin homology <IMM>  
Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 6 IGSWRFIRAFY 17  
DB 127 VGSDWRFRLRGYH 138  
RESULT 9  
137542  
MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A\*0216) precursor - hun  
C;Species: Homo sapiens (man)  
C;Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000  
A;Accession: I37542; S49582  
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.  
Immunogenetics 41, 388, 1995  
A;Title: Identification of a novel HLA-A2 subtype, HLA-A\*0216.  
A;Reference number: I37542; MUID:95278976; PMID:7759139  
A;Accession: I37542  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AA63; EMBL:Z46633; NID:G575248; PIDN:CAA86602.1; PID:  
A;Note: submitted to the EMBL Data Library, November 1994  
C;Genetics:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIMRPIRAF17  
Db 127 VGSDWRFRLRGYH 138  
: || ||| : : :  
: || ||| : : :

RESULT 10  
I84448  
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A\*02  
C;Species: Homo sapiens (man)  
A;Variety: isolate A\*0211  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 23-Jul-1999  
C;Accession: I84448  
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;  
Nature 357, 326-329, 1992  
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
A;Reference number: I37120; MUID:92269955; PMID:1317015  
A;Accession: I84448  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:G187623; PIDN:AAAS9603.1; PID:  
A;Experimental source: cell line GRC 138; isolate A\*0211  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: gp21.3-gp21.3  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;1-24/Domain: signal sequence  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predi  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIMRPIRAF17  
Db 127 VGSDWRFRLRGYH 138  
: || ||| : : :  
: || ||| : : :

RESULT 11  
I61857  
MHC HLA-A2.4a chain - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I61857  
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
J. Immunol. 142, 3937-3950, 1989  
A;Title: Diversity and diversification of HLA-A,B,C alleles.  
A;Reference number: I36956; MUID:89235215; PMID:2715640  
A;Accession: I61857  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016AD48; GB:M24042; NID:G187777; PIDN:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;

Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIMRPIRAF17  
Db 127 VGSDWRFRLRGYH 138  
: || ||| : : :  
: || ||| : : :

RESULT 12  
I38442  
gene HLA-A-0205 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I38442  
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.  
J. Immunol. 139, 936-941, 1987  
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28  
A;Reference number: I38441; MUID:87252273; PMID:3496393  
A;Accession: I38442  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:G432436; PIDN:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIMRPIRAF17  
Db 127 VGSDWRFRLRGYH 138  
: || ||| : : :  
: || ||| : : :

RESULT 13  
A34341  
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus  
C;Species: Alcaligenes eutrophus  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34341; A39190  
R;Peoples, O.P.; Sinskey, A.J.  
J. Biol. Chem. 264, 15298-15303, 1989  
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident  
A;Reference number: A34341; MUID:89359357; PMID:2670936  
A;Accession: A34341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-589 <PEO>  
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:G141958; PIDN:  
A;Experimental source: strain H16  
R;Schubert, P.; Krueger, N.; Steinbuechel, A.  
J. Bacteriol. 173, 168-175, 1991  
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt  
omoter.  
A;Reference number: A39190; MUID:91100279; PMID:1987116  
A;Accession: A39190  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-219 <SCH>  
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:G141964; PIDN:AAA21979.1; PID:  
A;Note: the authors translated the codon TAC for residue 120 as Thr  
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc  
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;  
Best Local Similarity 47.6%; Pred. No. 34;  
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RRFSGSIW-----RPIRAF17  
Db 100 RRFAGDAWRTNLPYRFAAFY 120  
: ||| : : :  
: ||| : : :

RESULT 14  
B81690  
probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) nqrB chain TC  
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: B81690  
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A;Reference number: A81500; MUID:20150255; PMID:10684935  
A;Accession: B81690  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-503 <TET>  
A;Cross-references: UNIPROT:Q9PKB6; UNIPARC:UPI0000057982; GB:AE002323; GB:AE002160; NID  
A;Experimental source: strain Nigg (MoPn)  
C;Genetics:  
A;Gene: TC0550  
C;Keywords: oxidoreductase

Query Match 43.9%; Score 43; DB 2; Length 503;  
Best Local Similarity 46.2%; Pred. No. 42;  
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 LRRFIGSIWRFIR 14  
DB 2 LEKFVDSLWKF 14  
  
RESULT 15  
T02263  
cytochrome P450 DWARF3 - maize  
N;Contains: oxidoreductase (EC 1.-.-.-)  
C;Species: Zea mays (maize)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T02263  
R;Winkler, R.G.; Helentjaris, T.  
Plant Cell 7, 1307-1317, 1995  
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberellin biosynthesis  
A;Reference number: Z14648; MUID:96004534; PMID:7549486  
A;Accession: T02263  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-519 <WIN>  
A;Cross-references: UNIPROT:Q43246; UNIPARC:UPI0000126CF8; EMBL:U32579; NID:g987266; PID  
A;Experimental source: strain B73  
C;Genetics:  
A;Gene: dwarf3  
C;Function:  
A;Description: involved in an early step in gibberellin biosynthesis  
A;Pathway: gibberellin biosynthesis  
C;Superfamily: Synchocystis cytochrome P450 slr0574; cytochrome P450 homology  
C;Keywords: oxidoreductase  
F;325-488/Domain: Cytochrome P450 homology <P45>

Query Match 43.9%; Score 43; DB 1; Length 519;  
Best Local Similarity 54.5%; Pred. No. 43;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 IGSIWRFIRAF 16  
DB 82 VGGWAFURAF 92  
  
Search completed: May 19, 2006, 14:39:58  
Job time : 14.2857 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds  
 (without alignments)  
 144.247 Million cell updates/sec

Title: US-10-712-447-115  
 Perfect score: 98  
 Sequence: 1 GLRRFIGSIWRFRATYFG 18

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Uniprot 7.2.\*  
 1: uniprot\_sprot.\*  
 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	54	55.1	670	2	Q25271_LRPDE	Q25271 leptinotars
2	54	55.1	805	2	Q3APY5_CHLCH	Q3APY5 chlorobium
3	51	52.0	488	2	Q84ZW1_PEA	Q84ZW1 pisum sativ
4	50	51.0	735	2	Q9F7V7_RHILV	Q9F7V7 rhizobium l
5	48	49.0	361	2	Q2NUB5_SODGL	Q2NUB5 sodalis glo
6	48	49.0	401	2	Q7NKK3_GLOVI	Q7NKK3 gloeobacter
7	48	49.0	449	2	Q3PK79_PARDE	Q3PK79 paracoccus
8	48	49.0	579	1	KKR7_HUMAN	Q5gh72 homo sapien
9	48	49.0	579	1	KKR7_PANTR	Q43lsl pan troglod
10	48	49.0	580	1	KKR7_MOUSE	Q5gh64 mus musculu
11	48	49.0	580	1	KKR7_RAT	Q5gh56 rattus norv
12	48	49.0	597	2	Q5AUS5_EMENI	Q5aus5 aspergillus
13	48	49.0	627	2	P74489_SVNY3	P74489 synecocyst
14	48	49.0	805	2	Q44QD1_CHLLI	Q44qd1 chlorobium
15	48	49.0	816	2	Q43K01_9CHLB	Q43k01 chlorobium
16	47	48.0	219	2	Q6LIT5_PICTO	Q6llt5 picrophilus
17	47	48.0	287	2	Q76442_CABEL	Q76442 caenorhabdi
18	47	48.0	407	2	Q39L57_BURS3	Q39l57 burkholderi
19	47	48.0	408	2	Q456F4_9BURK	Q456f4 burkholderi
20	47	48.0	408	2	Q4LK44_9BURK	Q4lk44 burkholderi
21	47	48.0	486	2	Q5U4I4_XENLA	Q5u4i4 xenopus lae
22	47	48.0	487	2	Q3ZN49_XENLA	Q3zn49 xenopus lae
23	47	48.0	506	2	Q5VRM7_ORISA	Q5vrm7 oryza sativ
24	47	48.0	607	2	Q425W5_DESHA	Q425w5 desulfitoba
25	46	46.9	426	2	Q99AQ7_9VIRU	Q99aq7 torque teno
26	46	46.9	578	1	KKR6_TETNG	Q49lsl tetraodon n
27	46	46.9	578	2	Q5GH49_FUGRU	Q5gh49 fugu rubrip
28	46	46.9	836	2	Q2Y8V4_NITMU	Q2y8v4 nitrospir
29	45	45.9	278	2	Q7VV93_BORPE	Q7vv93 bordetella
30	45	45.9	278	2	Q7WLP3_BORPA	Q7wlp3 bordetella
31	45	45.9	278	2	Q7WL31_BORBR	Q7wl31 bordetella

32	45	45.9	376	2	Q8KBA7_CHLTE	Q8kba7 chlorobium
33	45	45.9	406	2	Q56YS1_ARATH	Q56ys1 arabidopsis
34	45	45.9	409	2	Q4BFM2_BURVI	Q4bfm2 burkholderi
35	45	45.9	435	2	Q2JIT0_9CYAN	Q2jit0 cyanobacter
36	45	45.9	458	2	Q3M6C5_ANAVT	Q3m6c5 anabaena va
37	45	45.9	458	2	Q8XG08_TALSO	Q8xg08 ralsstonia s
38	45	45.9	489	1	KAO2_ARATH	Q9c5y2 arabidopsis
39	45	45.9	490	2	Q84ZW0_PEA	Q84zw0 pisum sativ
40	45	45.9	513	2	Q00857_FUSSP	Q00857 fusarium sp
41	45	45.9	519	2	Q9CIB7_FUSSP	Q9cib7 fusarium sp
42	45	45.9	540	2	Q5GH65_MOUSE	Q5gh65 mus musculu
43	45	45.9	580	2	Q5GH40_BRARE	Q5gh40 brachydanio
44	45	45.9	638	1	KKR6_RAT	Q5gh57 rattus norv
45	45	45.9	641	1	KKR6_HUMAN	Q5gh73 homo sapien

## ALIGNMENTS

RESULT 1  
 Q25271\_LRPDE PRELIMINARY; PRT; 670 AA.  
 AC Q25271\_LRPDE PRELIMINARY; PRT; 670 AA.  
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 25.  
 DE Diapause protein 1 (Fragment).  
 GN Name=Dp19;  
 OS Leptinotarsa decemlineata (Colorado potato beetle).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;  
 OC Leptinotarsa.  
 OC NCBI\_TaxID=7539;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA de Kort C.A.D., Koopmanschap A.B.;  
 RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding  
 diapause protein 1, an amylophorin-type storage hexamer of the Colorado  
 potato beetle.";  
 RT J. Insect Physiol. 40:527-535 (1994).  
 RL CC  
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EMBL; X76080; CAA53691.1; -; mRNA.  
 HSSP; P04253; 1LL1.  
 GO; GO:0005344; P:oxygen transporter activity; IEA.  
 GO; GO:0006810; P:transport; IEA.  
 InterPro; IPR000896; Hemocyanin.  
 InterPro; IPR005203; hemocyanin\_C.  
 InterPro; IPR005204; hemocyanin\_N.  
 PANTHER; PTHR11511; Hemocyanin; 1.  
 Pfam; PF03723; Hemocyanin\_C; 1.  
 Pfam; PF00372; Hemocyanin\_M; 1.  
 Pfam; PF03722; Hemocyanin\_N; 1.  
 PRINTS; PR00187; HAEMOCYANIN.  
 PROSITE; PS00210; HEMOCYANIN\_2; UNKNOWN\_1.  
 NON\_TER 1  
 SEQUENCE 670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;

Query Match 55.1%; Score 54; DB 2; Length 670;

Best Local Similarity 43.8%; Pred. No. 9.8;

Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFIGSIWRFRATYFG 18

Db 351 RKFYGALMSYLRHPFG 366

## RESULT 2

Q3APY5\_CHLCH PRELIMINARY; PRT; 805 AA.  
 ID Q3APY5\_CHLCH

GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR InterPro; IPR002401; EP450I.  
DR PANTHER; PTHR19383; Cytochrome\_P450; 1.  
DR Pfam; PF00067; P450; 2.  
DR PRINTS; PR00463; EP450I.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;  
KW Monooxygenase; Oxidoreductase.  
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6B43CB30 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 488;  
Best Local Similarity 66.7%; Pred.No. 21;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps

Qy 5 FTGSIWRFRAP 16  
Db 54 FIGNWSFLRAP 65  
||||| |||||

RESULT 4  
Q9FV7V\_RHLIV PRELIMINARY; PRT; 735 AA.  
AC Q9FV7V;  
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.  
DI 01-MAR-2001, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE ABC transporter RzcB.  
GN Name=rzcb;  
OS Rhizobium leguminosarum bv. viciae.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
CC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=387;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=305;  
RC MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;  
RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;  
RT "Analysis of the genetic region encoding a novel rhizobiocin from  
Rhizobium leguminosarum bv. viciae strain 305.";  
RL Can. J. Microbiol. 47:495-502(2001).  
CC

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EMBL; AF273216; AAC25076.1; -; Genomic\_DNA.  
DR HSSP; P08716; LMT0.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005224; F:ATP binding; IEA.  
DR GO; GO:0016987; F:ATPase activity; IEA.  
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m...; IEA  
DR GO; GO:0001666; F:nucleotide binding; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0008565; F:protein transporter activity; IEA.  
DR GO; GO:0015031; P:protein transport; IEA.  
DR GO; GO:0006508; P:proteolysis; IEA.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR011527; ABC\_TM\_1.  
DR InterPro; IPR001140; ABC\_TM\_transpt.  
DR InterPro; IPR001439; ABC\_transp\_like.  
DR InterPro; IPR005074; Peptidase\_C39.  
DR InterPro; IPR010132; Type\_I\_sec\_HlyB.  
DR PANTHER; PTHR19242:SF74; Type\_I\_sec\_HlyB; 1.  
DR Pfam; PF00664; ABC\_membrane; 1.  
DR Pfam; PF00005; ABC\_tran; 1.  
DR Pfam; PF03412; Peptidase\_C39; 1.  
DR ProDom; PD000006; ABC\_transporter; 1.  
DR SMART; SM00382; AAA; 1.  
DR TIGRFAMs; TIGR01846; type\_I\_sec\_HlyB; 1.  
DR PROSITE; PS00929; ABC\_TMIF; 1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.

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DR PROSITE; PS0990; PEPTIDASE C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 51.0%; Score 50; DB 2; Length 735;
Best Local Similarity 56.2%; Pred. No. 47;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAF 16
DB 161 GFRWFLPAIWRYRRAP 176

RESULT 5
Q2NUB5_SODGL
ID Q2NUB5_SODGL PRELIMINARY; PRT; 361 AA.
AC Q2NUB5;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Putative glycosyltransferase.
GN ORFNames=SG0985;
OS Sodalis glossinidius str. 'morsitans'.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=343509;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Morsitans;
RA Toh H., Weiss B.B., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RA "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156(2006).
CC
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CC
CC EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
DR TRANSFERASE.
KW SEQUENCE 361 AA; 40247 MW; 1557F70F3C3CA6EC CRC64;

Query Match 49.0%; Score 48; DB 2; Length 361;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RFIGSIWRFIRAF 16
DB 62 RDVGFWRFILSAF 74

RESULT 6
Q7NWK3_GLOVI
ID Q7NWK3_GLOVI PRELIMINARY; PRT; 401 AA.
AC Q7NWK3;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Gll1363 protein.
GN OrderedLocusNames=gll1363;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kiehida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpō S.,
RA Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
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RL DNA Res. 10:137-145(2003).
CC
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CC
CC EMBL; BA000445; BAC89304.1; -; Genomic_DNA.
DR BIOCYC; GVIO251221:GLU1363-MONOMER; -.
DR GO; GO:0004040; F:amidase activity; IEA.
DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3_hydro.
DR InterPro; IPR002901; Amidase_4.
DR Pfam; PF01520; Amidase_3; 1.
DR Pfam; PF01832; Glucosaminidase; 1.
KW Complete proteome.
SQ SEQUENCE 401 AA; 44051 MW; 903814BB688C170B CRC64;

Query Match 49.0%; Score 48; DB 2; Length 401;
Best Local Similarity 69.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFI 13
DB 104 GLERFIRGYWRFI 116

RESULT 7
Q3PK79_PARDE
ID Q3PK79_PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
GN ORFNames=PdenDRAFT_4722;
OS Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=318586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Paracoccus
RT denitrificans PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Paracoccus denitrificans
RT PD1222.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC -! SIMILARITY: Belongs to the cytochrome P450 family.
CC
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CC
CC EMBL; AA101000001; EAM68115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; p450; 1.
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DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3EBC9E12AA3B35 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 449;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSIWRFIRAF 16
Db 13 GSVWRFIRDF 22

RESULT 8
XKR7 HUMAN
ID XKR7 HUMAN STANDARD; PRT; 579 AA.
AC QSGH72; Q9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=C20orf159, XRG7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burzell W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
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CC
DR EMBL; AV534245; AAT07094.1; -; mRNA.
DR EMBL; AL031658; CAB88102.1; ALT_SEQ; Genomic DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
DR HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF64B9EDD53D CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAF 17
Db 190 LGQWRYLRALY 201

RESULT 9
XKR7 PANTR
ID XKR7 PANTR STANDARD; PRT; 579 AA.
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC
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CC
DR EMBL; AV702910; AAV83783.1; -; mRNA.
KW Membrane; Transmembrane.
SQ SEQUENCE 579 AA; 63593 MW; 6DFF1191093E85D4 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAF 17
Db 190 LGQWRYLRALY 201
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RESULT 10
XKR7 MOUSE
ID   XKR7 MOUSE          STANDARD;          PRT;   580 AA.
AC   Q5GH64;
DT   11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DI   01-MAR-2005, sequence version 1.
DI   07-FEB-2006, entry version 10.
DE   XK-related protein 7.
GN   Name=Xkr7; Synonyms=Xrg7;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=C57BL/6J;
RA   Huang C.-H., Chen Y.;
RT   "A superfamily of XK-related genes (XRG) widely expressed in
RT   vertebrates and invertebrates.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC   (Potential).
CC   -!- SIMILARITY: Belongs to the XK family.
CC   -----
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CC   -----
EMBL: AY534253; AAT07102.1; -; mRNA.
DR   EMBL; ENSMUSG0000042631; Mus musculus.
DR   MGI; MGI:3526711; Xkr7.
KW   Membrane; Transmembrane.
CHAIN 1 580
FT   FTID=PRO_0000190789.
FT   TRANSMEM 59 79
FT   TRANSMEM 89 109
FT   TRANSMEM 260 280
FT   TRANSMEM 303 323
FT   TRANSMEM 326 346
FT   TRANSMEM 355 375
FT   TRANSMEM 384 404
FT   TRANSMEM 415 435
SQ   SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 580;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 6 IGSWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 11
XKR7 RAT
ID   XKR7 RAT            STANDARD;          PRT;   580 AA.
AC   Q5GH56;
DT   11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DI   01-MAR-2005, sequence version 1.
DI   07-FEB-2006, entry version 8.
DE   XK-related protein 7.
GN   Name=Xkr7; Synonyms=Xrg7;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
[1]
NUCLEOTIDE SEQUENCE [MRNA].
STRAIN=Sprague-Dawley;
RA   Huang C.-H., Chen Y.;

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RT   "A superfamily of XK-related genes (XRG) widely expressed in
RT   vertebrates and invertebrates.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC   (Potential). Belongs to the XK family.
CC   -----
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CC   -----
EMBL: AY534261; AAT07110.1; -; mRNA.
DR   EMBL; AY534261; AAT07110.1; -; mRNA.
KW   Membrane; Transmembrane.
CHAIN 1 580
FT   FTID=PRO_0000190791.
FT   TRANSMEM 59 79
FT   TRANSMEM 89 109
FT   TRANSMEM 260 280
FT   TRANSMEM 303 323
FT   TRANSMEM 326 346
FT   TRANSMEM 355 375
FT   TRANSMEM 384 404
FT   TRANSMEM 415 435
SQ   SEQUENCE 580 AA; 64338 MW; 3F4907F391B4F5BE CRC64;

Query Match 49.0%; Score 48; DB 1; Length 580;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 6 IGSWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 12
Q5AUS5_EMENI
ID   Q5AUS5_EMENI        PRELIMINARY;      PRT;   597 AA.
AC   Q5AUS5;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
DI   26-APR-2005, sequence version 1.
DI   07-MAR-2006, entry version 6.
DE   Hypothetical protein.
GN   ORFNames=AN7955.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OC   NCBI_TaxID=227321;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=FGSC 4;
PubMed=16372000; DOI=10.1038/nature04341;
RA   Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA   Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
RA   Kapitonov V., Jurka J., Scaccocchio C., Farman M., Butler J.,
RA   Puccinelli S., Harris S., Braus G.H., Drant O., Busch S., D'Enfert C.,
RA   Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA   Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
RA   Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA   Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
RA   Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
RA   Sachs M.S., Osmani S.A., Birren B.W.;
RT   "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT   fumigatus and A. oryzae.";
RL   Nature 438:1105-1115 (2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC   preliminary data.
CC   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
CC   -----
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CC   -----
EMBL: AACD01000135; EAA59609.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0015205; F:nucleobase transporter activity; IEA.

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RC STRAIN-DSM 245;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RT Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium limicola
RT DSM 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-DSM 245;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium limicola DSM
RT 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAHQ01000009; EAM43320.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Lev tRNAAsn_1a.
DR Pfam; PF00133; tRNA-synt_1_1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
DR Aminoacyl-tRNA synthetase.
KW SEQUENCE 805 AA; 91997 MW; D4F3FE28F9B52DF3 CRC64;
SQ
Query Match 49.0%; Score 48; DB 2; Length 805;
Best Local Similarity 46.2%; Pred.No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps
QY 1 GLRRFIGSIWRFI 13
|:|:|:|:|:
Db 622 GISRFLGKVRLLV 634

RESULT 15
ID Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC Q43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GS ORFNames=Cpha266DRAFT_2546;
GN Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxId=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RT Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAHQ01000009; EAM43320.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Lev tRNAAsn_1a.
DR Pfam; PF00133; tRNA-synt_1_1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
DR Aminoacyl-tRNA synthetase.
KW SEQUENCE 805 AA; 91997 MW; D4F3FE28F9B52DF3 CRC64;
SQ

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CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0004823; P:leucine-tRNA ligase activity; IEA.
DR      GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR      InterPro; IPR002302; Leu_tRNAasn_1a.
DR      Pfam; PF00133; tRNA-synt_1; 1.
DR      PRINTS; PR00985; TRNASYNTHLEU.
DR      TIGRFAMs; TIGR00396; leus_bact; 1.
KW      Aminoacyl-tRNA synthetase_
SQ      SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 816;
Best Local Similarity 46.2%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy      1 GLRRFIGSIWRFI 13
Db      622 GISRFLGKVKVRLV 634
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Search completed: May 19, 2006, 14:38:14  
Job time : 115.429 secs

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Query Match 75.5%; Score 74; DB 2; Length 18;  
 Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
 Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFVG 18  
 |:::|:::|:::|:::|:::|  
 Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2  
 US-08-940-093-242  
 ; Sequence 242, Application US/08940093  
 ; Patent No. 6037323  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dasseux, Jean-Louis  
 ; APPLICANT: Sekul, Renate  
 ; APPLICANT: Buttner, Klaus  
 ; APPLICANT: Cornut, Isabelle  
 ; APPLICANT: Metz, Gunther  
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
 ; NUMBER OF SEQUENCES: 258  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/940,093  
 ; FILING DATE: 29-SEP-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 009196-0006-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-493-4935  
 ; TELEFAX: 650-493-5556  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 242:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: No. 6037323e  
 ; US-08-940-093-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
 Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
 Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFVG 18  
 |:::|:::|:::|:::|:::|  
 Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3  
 US-08-940-096-242  
 ; Sequence 242, Application US/08940096  
 ; Patent No. 6046166  
 ; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis  
 ; APPLICANT: Sekul, Renate  
 ; APPLICANT: Buttner, Klaus  
 ; APPLICANT: Cornut, Isabelle  
 ; APPLICANT: Metz, Gunther  
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
 ; NUMBER OF SEQUENCES: 258  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/940,096  
 ; FILING DATE: 29-SEP-1997  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 009196-0005-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-493-4935  
 ; TELEFAX: 650-493-5556  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 242:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: No. 6046166e  
 ; US-08-940-096-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
 Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
 Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFVG 18  
 |:::|:::|:::|:::|:::|  
 Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4  
 US-09-465-719-242  
 ; Sequence 242, Application US/09465719  
 ; Patent No. 6265377  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dasseux, Jean-Louis  
 ; APPLICANT: Sekul, Renate  
 ; APPLICANT: Buttner, Klaus  
 ; APPLICANT: Cornut, Isabelle  
 ; APPLICANT: Metz, Gunther  
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
 ; NUMBER OF SEQUENCES: 258  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIKAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-605-242
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; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIKAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-838-242
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US-09-453-838-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFTAFYV 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFV 18

## RESULT 7

US-08-940-136-242

; Sequence 242, Application US/08940136  
; Patent No. 6518412  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Metz, Isabelle  
; APPLICANT: Cornut, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO  
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR  
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,136  
; FILING DATE: 29-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0007-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6518412e

US-08-940-136-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFTAFYV 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFV 18

## RESULT 8

US-09-453-841-242

; Sequence 242, Application US/09453841

; Patent No. 6573239  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/453,841  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/940,095  
; FILING DATE: 29-SEP-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6573239e

US-09-453-841-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFTAFYV 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFV 18

## RESULT 9

US-09-453-833-242

; Sequence 242, Application US/09453833  
; Patent No. 6602854  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Buttner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP



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; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; US-09-453-833-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 10
US-09-453-826-242
; Sequence 242, Application US/09453826
; Patent No. 6630450
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.  
;; NUMBER OF SEQUENCES: 274  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: NY  
;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

;; US-10-283-599-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRPIRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

;; Sequence 242, Application US/09465718

;; Patent No. 6900177

;; GENERAL INFORMATION:

;; APPLICANT: Dasseux, Jean-Louis

;; APPLICANT: Sekul, Renate

;; APPLICANT: Buttner, Klaus

;; APPLICANT: Cornut, Isabelle

;; APPLICANT: Metz, Gunther

;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

;; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

;; NUMBER OF SEQUENCES: 258

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718  
;; FILING DATE: 17-Dec-1999  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/940,096  
;; FILING DATE: 29-SEP-1997  
;; APPLICATION NUMBER:  
;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

;; US-09-465-718-242

Query Match 75.5%; Score 74; DB 2; Length 18;

Best Local Similarity 61.1%; Pred. No. 3.9e-05;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRPIRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55

Job time : 24.8571 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 seconds  
(without alignments)

102.575 Million cell updates/sec

Title: US-10-712-447-115

Perfect score: 98

Sequence: 1 GLRRFIGSIWRIFAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-115
2	98	100.0	18	4	US-10-712-447-116
3	94	95.9	18	4	US-10-712-447-2
4	94	95.9	18	4	US-10-712-447-5
5	94	95.9	18	4	US-10-712-447-8
6	94	95.9	18	4	US-10-712-447-10
7	94	95.9	18	4	US-10-712-447-13
8	94	95.9	18	4	US-10-712-447-117
9	94	95.9	18	4	US-10-712-447-127
10	94	95.9	18	4	US-10-712-447-131
11	91	92.9	18	4	US-10-712-447-91
12	90	91.8	18	4	US-10-712-447-129
13	88	89.8	18	4	US-10-712-447-21
14	88	89.8	18	4	US-10-712-447-53
15	88	89.8	18	4	US-10-712-447-74
16	86	87.8	18	4	US-10-712-447-4
17	86	87.8	18	4	US-10-712-447-112
18	85	86.7	18	4	US-10-712-447-99
19	84	85.7	18	4	US-10-712-447-18
20	84	85.7	18	4	US-10-712-447-113
21	84	85.7	18	4	US-10-712-447-114
22	83	84.7	18	4	US-10-712-447-17
23	83	84.7	18	4	US-10-712-447-121
24	82	83.7	18	4	US-10-712-447-61
25	82	83.7	18	4	US-10-712-447-82
26	81	82.7	18	4	US-10-712-447-16
27	81	82.7	18	4	US-10-712-447-96

Sequence 22, Appl  
Sequence 78, Appl  
Sequence 95, Appl  
Sequence 120, Appl  
Sequence 19, Appl  
Sequence 56, Appl  
Sequence 58, Appl  
Sequence 77, Appl  
Sequence 80, Appl  
Sequence 94, Appl  
Sequence 97, Appl  
Sequence 242, Appl  
Sequence 242, Appl

#### ALIGNMENTS

RESULT 1  
US-10-712-447-115  
; Sequence 115, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 115  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-115

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFYG 18  
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Db 1 GLRRFIGSIWRIFAFYG 18

RESULT 2  
US-10-712-447-116  
; Sequence 116, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13



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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 7
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 8
US-10-712-447-117
; Sequence 117, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-117

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFYG 18
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Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 9
US-10-712-447-127
; Sequence 127, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 127
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-127

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFYG 18
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Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 10
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131
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Search completed: May 19, 2006, 15:27:57  
Job time : 81.2857 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds  
(without alignments)  
17.943 Million cell updates/sec

Title: US-10-712-447-115

Perfect score: 98

Sequence: 1 GLRRFIGSIWRPFAVFG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pap.\*
- 2: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*
- 5: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pap.\*
- 6: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	38.8	74	1	US-09-949-925-111
2	37.5	38.3	441	6	US-10-511-937-2947
3	35	35.7	651	6	US-10-511-937-2401
4	34.5	35.2	60	1	US-09-949-925-142
5	34	34.7	522	6	US-10-505-928-543
6	34	34.7	599	7	US-11-302-678-5
7	33.5	34.2	244	7	US-11-169-140-109
8	33.5	34.2	503	7	US-11-024-544A-21
9	33.5	34.2	503	7	US-11-190-750-135
10	33.5	34.2	503	7	US-11-264-784-87
11	33	33.7	313	7	US-11-242-505A-48
12	33	33.7	342	7	US-11-204-427-7
13	33	33.7	393	7	US-11-304-129-40
14	33	33.7	393	7	US-11-304-129-48
15	33	33.7	403	7	US-11-242-505A-18
16	33	33.7	463	6	US-10-505-928-545
17	33	33.7	643	6	US-10-504-120-19
18	33	33.7	667	7	US-11-311-555-16
19	33	33.7	667	7	US-11-311-561-16
20	33	33.7	714	6	US-10-868-498-2
21	33	33.7	919	7	US-11-302-678-62
22	32	32.7	351	6	US-10-511-937-2540
23	32	32.7	364	7	US-11-113-081A-6
24	32	32.7	388	6	US-10-196-749-336
25	32	32.7	388	7	US-11-024-544A-169

ALIGNMENTS

RESULT 1  
US-09-949-925-111  
; Sequence 111, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (74)  
; OTHER INFORMATION: Xaa equals stop translation  
; US-09-949-925-111

Query Match 38.8%; Score 38; DB 1; Length 74;  
Best Local Similarity 63.6%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 LRRFIGSIWRP 12

||| |||||

Sequence 137, App  
Sequence 1, Appli  
Sequence 12, Appl  
Sequence 17, Appl  
Sequence 859, App  
Sequence 88, Appl  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 569, App  
Sequence 23, Appl  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 24, Appl  
Sequence 25, Appl  
Sequence 26, Appl  
Sequence 6, Appli  
Sequence 18, Appl  
Sequence 3, Appli



; PRIOR APPLICATION NUMBER: US 60/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO 543  
 ; LENGTH: 522  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;  
 Best Local Similarity 47.1%; Pred. No. 55;  
 Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 3 RRFI--GSIWRFIRAFY 17  
 ||| :|:|:|:|  
 Db 473 RRFTQSGDLYNRHRRKFH 489

RESULT 6  
 US-11-302-678-5  
 ; Sequence 5, Application US/11302678  
 ; Publication No. US20060088881A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Silos-Santiago, Inmaculada  
 ; APPLICANT: Venkateswarlu, Karicheti  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,  
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
 ; FILE REFERENCE: MP102-012P1RM OMNI  
 ; CURRENT APPLICATION NUMBER: US711/302,678  
 ; CURRENT FILING DATE: 2005-12-14  
 ; PRIOR APPLICATION NUMBER: US/10/345,680  
 ; PRIOR FILING DATE: 2003-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/349,511  
 ; PRIOR FILING DATE: 2002-01-18  
 ; PRIOR APPLICATION NUMBER: US 60/360,500  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/365,041  
 ; PRIOR FILING DATE: 2002-03-15  
 ; PRIOR APPLICATION NUMBER: US 60/374,063  
 ; PRIOR FILING DATE: 2002-04-19  
 ; PRIOR APPLICATION NUMBER: US 60/403,468  
 ; PRIOR FILING DATE: 2002-08-14  
 ; PRIOR APPLICATION NUMBER: US 60/414,262  
 ; PRIOR FILING DATE: 2002-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/419,986  
 ; PRIOR FILING DATE: 2002-10-21  
 ; PRIOR APPLICATION NUMBER: US 60/423,809  
 ; PRIOR FILING DATE: 2002-11-05  
 ; PRIOR APPLICATION NUMBER: US 60/429,797  
 ; PRIOR FILING DATE: 2002-11-26  
 ; NUMBER OF SEQ ID NOS: 66  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 599  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-11-302-678-5

Query Match 34.7%; Score 34; DB 7; Length 599;  
 Best Local Similarity 57.1%; Pred. No. 64;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IGS1WRF 12  
 :|:|:|:|  
 Db 64 LGVWRF 70

RESULT 7  
 US-11-169-140-109

; Sequence 109, Application US/11169140  
 ; Publication No. US20060099150A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.  
 ; APPLICANT: HOUSTON, Lou, L.  
 ; APPLICANT: SHERIDAN, Philip, J.  
 ; APPLICANT: HAWLEY, Stephen  
 ; APPLICANT: GLYNN, Jacqueline, M.  
 ; APPLICANT: CHAPIN, Steven  
 ; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI  
 ; TITLE OF INVENTION: BARRIERS  
 ; FILE REFERENCE: 11474-037-999  
 ; CURRENT APPLICATION NUMBER: US/11/169,140  
 ; CURRENT FILING DATE: 2005-06-27  
 ; PRIOR APPLICATION NUMBER: US 60/267,601  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/248,819  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/248,478  
 ; PRIOR FILING DATE: 2000-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/237,929  
 ; PRIOR FILING DATE: 2000-10-02  
 ; PRIOR APPLICATION NUMBER: 09/949,039  
 ; PRIOR FILING DATE: 2001-09-06  
 ; PRIOR APPLICATION NUMBER: 09/969,748  
 ; PRIOR FILING DATE: 2001-10-02  
 ; NUMBER OF SEQ ID NOS: 143  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 109  
 ; LENGTH: 244  
 ; TYPE: PRT  
 ; ORGANISM: Simian  
 US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;  
 Best Local Similarity 42.1%; Pred. No. 27;  
 Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

Qy 1 GLRRFIGSIW-----RPIR 14  
 || :|:|:|:|  
 Db 158 GLVLALGAVWCVARPIR 176

RESULT 8  
 US-11-024-544A-21  
 ; Sequence 21, Application US/11024544A  
 ; Publication No. US20060094086A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
 ; APPLICANT: Yadav, Narendra  
 ; APPLICANT: Xue, Zhixiong  
 ; APPLICANT: Zhang, Hongxiang  
 ; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED  
 ; TITLE OF INVENTION: FATTY ACIDS AND OIL CONTENT IN OLEAGINOUS ORGANISMS  
 ; FILE REFERENCE: CL2717  
 ; CURRENT APPLICATION NUMBER: US/11/024,544A  
 ; CURRENT FILING DATE: 2004-12-29  
 ; NUMBER OF SEQ ID NOS: 175  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 21  
 ; LENGTH: 503  
 ; TYPE: PRT  
 ; ORGANISM: Magnaporthe grisea 70-15  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: GenBank Accession No. EAA52634  
 ; DATABASE ENTRY DATE: 2003-10-31  
 ; RELEVANT RESIDUES: (1)..(503)  
 US-11-024-544A-21

Query Match 34.2%; Score 33.5; DB 7; Length 503;  
 Best Local Similarity 43.8%; Pred. No. 64;  
 Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18  
|||: ||: | : | : |  
Db 156 RRFV-STWKLIALVHG 170

RESULT 9  
US-11-190-750-135  
; Sequence 135, Application US/11190750  
; Publication No. US20060094089A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Yadav, Narendra  
; APPLICANT: Zhang, Hongxiang  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS TO INCREASE THE PERCENT OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF  
; FILE REFERENCE: CL2718  
; CURRENT APPLICATION NUMBER: US/11/190,750  
; CURRENT FILING DATE: 2005-07-27  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 135  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]  
US-11-190-750-135

Query Match 34.2%; Score 33.5; DB 7; Length 503;  
Best Local Similarity 43.8%; Pred. No. 64;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18  
|||: ||: | : | : |  
Db 156 RRFV-STWKLIALVHG 170

RESULT 10  
US-11-264-784-87  
; Sequence 87, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Raghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 87  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: DGAT1  
US-11-264-784-87

Query Match 34.2%; Score 33.5; DB 7; Length 503;  
Best Local Similarity 43.8%; Pred. No. 64;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18

Db 156 RRFV-STWKLIALVHG 170  
|||: ||: | : | : |

RESULT 11  
US-11-242-505A-48  
; Sequence 48, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Hematological Disorders for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c  
; FILE REFERENCE: MPI2001-288P1RCPIONNIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-242-505A-48

Query Match 33.7%; Score 33; DB 7; Length 313;  
Best Local Similarity 62.5%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 WRFIRAFY 17  
||: ||: ||  
Db 199 WSFLDAFY 206

RESULT 12  
US-11-204-427-7  
; Sequence 7, Application US/11204427  
; Publication No. US20060100146A1  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L  
; APPLICANT: Turkish, Aaron R  
; APPLICANT: Billheimer, Jeffrey T  
; APPLICANT: Cromley, Debra  
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES  
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS  
; CURRENT APPLICATION NUMBER: US/11/204,427  
; CURRENT FILING DATE: 2005-08-15  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;  
Best Local Similarity 50.0%; Pred. No. 50;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17  
: ||: ||: ||  
Db 84 AIWQRUDYY 93

RESULT 13

US-11-304-129-40  
 ; Sequence 40, Application US/11304129  
 ; Publication No. US20060088915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OHTAKI, Tetsuya  
 ; APPLICANT: MASUDA, Yasushi  
 ; APPLICANT: TAKATSU, Yoshihiro  
 ; APPLICANT: WATANABE, Takuya  
 ; APPLICANT: TERAQ, Yasuko  
 ; APPLICANT: SHINTANI, Yasushi  
 ; APPLICANT: HINUMA, Syuji  
 ; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
 ; FILE REFERENCE: 2762USOP  
 ; CURRENT APPLICATION NUMBER: US/11/304,129  
 ; CURRENT FILING DATE: 2005-12-15  
 ; PRIOR APPLICATION NUMBER: US/10/333,192  
 ; PRIOR FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: JP 2000-217442  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: JP 2001-26779  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
 ; PRIOR FILING DATE: 2001-07-17  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SEQ ID NO 40  
 ; LENGTH: 393  
 ; TYPE: PRT  
 ; ORGANISM: Rat  
 ; ORGANISM: Mouse  
 US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;  
 Best Local Similarity 46.2%; Pred. No. 58;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 FIGSIWRFIRAFY 17  
 Db 216 FCGIWPVDQFY 228

RESULT 14  
 US-11-304-129-48  
 ; Sequence 48, Application US/11304129  
 ; Publication No. US20060088915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OHTAKI, Tetsuya  
 ; APPLICANT: MASUDA, Yasushi  
 ; APPLICANT: TAKATSU, Yoshihiro  
 ; APPLICANT: WATANABE, Takuya  
 ; APPLICANT: TERAQ, Yasuko  
 ; APPLICANT: SHINTANI, Yasushi  
 ; APPLICANT: HINUMA, Syuji  
 ; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
 ; FILE REFERENCE: 2762USOP  
 ; CURRENT APPLICATION NUMBER: US/11/304,129  
 ; CURRENT FILING DATE: 2005-12-15  
 ; PRIOR APPLICATION NUMBER: US/10/333,192  
 ; PRIOR FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: JP 2000-217442  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: JP 2001-26779  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
 ; PRIOR FILING DATE: 2001-07-17  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SEQ ID NO 48  
 ; LENGTH: 393  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;  
 Best Local Similarity 46.2%; Pred. No. 58;  
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FIGSIWRFIRAFY 17  
 Db 216 FCGIWPVDQFY 228

RESULT 15  
 US-11-242-505A-18  
 ; Sequence 18, Application US/11242505A  
 ; Publication No. US20060099656A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carroll, Joseph M.  
 ; APPLICANT: Healy, Aileen  
 ; TITLE OF INVENTION: Methods and Compositions for Treating  
 ; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
 ; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
 ; FILE REFERENCE: MPI2001-288P1RCP10WNIM  
 ; CURRENT APPLICATION NUMBER: US/11/242,505A  
 ; CURRENT FILING DATE: 2005-10-03  
 ; PRIOR APPLICATION NUMBER: US 10/290,078  
 ; PRIOR FILING DATE: 2002-11-07  
 ; PRIOR APPLICATION NUMBER: US 60/347,949  
 ; PRIOR FILING DATE: 2001-11-07  
 ; PRIOR APPLICATION NUMBER: US 10/320,351  
 ; PRIOR FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: 60/341,606  
 ; PRIOR FILING DATE: 2001-12-17  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 18  
 ; LENGTH: 403  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; ORGANISM: Homo Sapiens  
 US-11-242-505A-18

Query Match 33.7%; Score 33; DB 7; Length 403;  
 Best Local Similarity 44.4%; Pred. No. 60;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LRRFIGSIW 10  
 Db 155 VRRVLGAVW 163

Search completed: May 19, 2006, 15:28:18  
 Job time : 2.14286 secs

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OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds  
(without alignments)  
87.287 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFGSIWRIFAFYK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34338	Synthetic
2	98	100.0	18	ADO34339	Synthetic
3	94	95.9	18	ADO34231	Synthetic
4	94	95.9	18	ADO34354	Synthetic
5	94	95.9	18	ADO34225	Synthetic
6	94	95.9	18	ADO34228	Synthetic
7	94	95.9	18	ADO34236	Synthetic
8	94	95.9	18	ADO34340	Synthetic
9	94	95.9	18	ADO34233	Synthetic
10	94	95.9	18	ADO34350	Synthetic
11	91	92.9	18	ADO34314	Synthetic
12	90	91.8	18	ADO34352	Synthetic
13	88	89.8	18	ADO34297	Synthetic
14	88	89.8	18	ADO34244	Synthetic
15	88	89.8	18	ADO34276	Synthetic
16	86	87.8	18	ADO34227	Synthetic
17	86	87.8	18	ADO34335	Synthetic
18	85	86.7	18	ADO34322	Synthetic
19	84	85.7	18	ADO34336	Synthetic
20	84	85.7	18	ADO34337	Synthetic
21	84	85.7	18	ADO34241	Synthetic
22	83	84.7	18	ADO34240	Synthetic
23	83	84.7	18	ADO34344	Synthetic

24	82	83.7	18	8	ADO34284	Synthetic
25	82	83.7	18	8	ADO34305	Synthetic
26	81	82.7	18	8	ADO34239	Synthetic
27	81	82.7	18	8	ADO34319	Synthetic
28	80	81.6	18	8	ADO34245	Synthetic
29	80	81.6	18	8	ADO34301	Synthetic
30	80	81.6	18	8	ADO34343	Synthetic
31	80	81.6	18	8	ADO34318	Synthetic
32	78	79.6	18	8	ADO34302	Synthetic
33	78	79.6	18	8	ADO34279	Synthetic
34	78	79.6	18	8	ADO34303	Synthetic
35	78	79.6	18	8	ADO34242	Synthetic
36	78	79.6	18	8	ADO34300	Synthetic
37	78	79.6	18	8	ADO34281	Synthetic
38	78	79.6	18	8	ADO34317	Synthetic
39	77	78.6	18	8	ADO34323	Synthetic
40	77	78.6	18	8	ADO34280	Synthetic
41	76	77.6	18	8	ADO34264	Synthetic
42	76	77.6	18	8	ADO34342	Synthetic
43	75	76.5	18	8	ADO34320	Synthetic
44	74	75.5	18	2	AA118917	Lecithin:
45	74	75.5	18	2	AA119171	Lecithin:

#### ALIGNMENTS

##### RESULT 1

ID ADO34338 standard; peptide; 18 AA.

AC ADO34338;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.

apolipoprotein-E mimicking polypeptide; antilipemic; cardiact; vasotropic; antiarteriosclerotic; cerebroprotective; antianginal; serum cholesterol; coronary artery disease; dysbetalipoproteinemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAFYG 18  
 |||||  
 Db 1 GLRRFIGSIWRFIRAFYG 18

## RESULT 2

ADO34339  
 ID ADO34339 standard; peptide; 18 AA.

AC ADO34339;  
 XX

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAFYG 18  
 |||||  
 Db 1 GLRRFIGSIWRFIRAFYG 18

## RESULT 3

ADO34231  
 ID ADO34231 standard; peptide; 18 AA.

AC ADO34231;  
 XX

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,

CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRIFAFYVG 18  
 |.|||.|||||||  
 Db 1 GRRFLGSIWRIFAFYVG 18

RESULT 4  
 ADO34354  
 ID ADO34354 standard; peptide; 18 AA.

XX  
 AC ADO34354;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 131; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRIFAFYVG 18  
 |.|||.|||||||  
 Db 1 GLRRFLGSIWRIFAFYVG 18

RESULT 5  
 ADO34225  
 ID ADO34225 standard; peptide; 18 AA.

XX  
 AC ADO34225;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 18

FT /note= "C-terminal amide"

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 2; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRRIRAFYG 18  
 Db 1 GIRFLGSIWRRIRAFYG 18

RESULT 6  
 ADO34228  
 ID ADO34228 standard; peptide; 18 AA.

XX  
 AC ADO34228;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 5.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 5; 79pp; English.

XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRRIRAFYG 18  
 Db 1 GIRFLGSIWRRIRAFYG 18

RESULT 7  
 ADO34236  
 ID ADO34236 standard; peptide; 18 AA.

XX  
 AC ADO34236;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 13; 79pp; English.

XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFIRAFYG 18  
 |:|||||:|||||:  
 Db 1 GIRRFGLSIWRIFIRAFYG 18

RESULT 8  
 ADO34340  
 ID ADO34340 standard; peptide; 18 AA.

XX  
 AC ADO34340;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFIRAFYG 18  
 |:|||||:|||||:  
 Db 1 GIRRFGLSIWRIFIRAFYG 18

RESULT 9  
 ADO34233  
 ID ADO34233 standard; peptide; 18 AA.

XX  
 AC ADO34233;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector a host cell, a recombinant cell or a transgenic, non-human subject comprising the synthetic apolipoprotein-E mimicking polypeptide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

Query Match	91.8%;	Score 90;	DB 8;	Length 18;
Best Local Similarity	77.8%;	Pred. No. 8.9e-07;		
Matches 14;	Conservative 4;	Mismatches 0;	Indels 0;	Gaps 0;

**Qy** 1 GRRFGSIWRIRAFYG 18  
1 : : : : : : : :  
**Dd** 1 GRRFLGSLWRRLAFYG 18

RESULT 13  
ADO34297  
ID ADO34297 standard; peptide: 18 AA.

AC ADO34297;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant; KW  
asotropic; antiarteriosclerotic; cerebroprotective; antilanginal; KW  
sarum cholesterol; coronary artery disease; dysbetalipoproteinaemia; KW  
atherosclerosis; myocardial infarction; stroke; embolus; angina; KW  
low-density lipoprotein. LDL; very-low density lipoprotein: VLDL; KW

OS Synthetic.

PN WO2004043403-A2.

PD 27-MAY-2004.

XX  
PF 13-NOV-2003; 2003WO-US036268.

XX  
PR 13-NOV-2002: 2002US-0425821P.

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PA (HARR-) HARR RES FOUND.

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PT Anantharamiah GM. Garber DW. Datta G:

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DB WPT: 2004-411629/38

**XX**

**synthetic angiotensin-E mimicking polypeptide useful for treating**

**PM**

PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
nm characterized an amino acid sequence

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The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: anti-lipemic, cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and anti-angiatic. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

Query Match 89.8%; Score 88; DB 8; Length 18;  
Best Local Similarity 77.8%; Pred. No. 1.8e-06;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18  
| : | : | : | : | : | :  
Db 1 GIRQFLGSIWRFIRAFYG 18

RESULT 14  
ADO34244  
ID ADO34244 standard; peptide; 18 AA.

AC ADO34244:

12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEO ID No 21.

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002: 2002US-0425821P.

PA (UABR-) UAB RES FOUND.

XX  
PI Anantharamiah GM. Garber DW. Datta G:

XX  
DR WPI: 2004-411629/38.

AA Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
PT  
PT comprises an amino acid sequence

XX  
PS Claim 4: SEQ ID NO 21: 79pp: English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape, chimpanzee or orangutan); for treating coronary artery disease,

CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

Sequence 18 AA:

Query Match	89.8%	Score 88;	DB 8;	Length 18;
Best Local Similarity	77.8%	Pred. No. 1.8e-06;		
Matches 14;	Conservative	4;	Mismatches 0;	Indels 0;
Gaps 0;				

Qy 1 GLRRFIGSIWRFIRAFYG 18  
| : | | : | | | | : | |  
Db 1 GRRFLGAIWRFI RSYFG 18

RESULT 15  
ADO34276

ID ADO34276 standard; peptide; 18 AA.

AC ADO34276;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.

apolipoprotein-E mimicking polypeptide; antilipemic; cardiac; vasotropic; antiarteriosclerotic; cerebroprotective; antilanginal; serum cholesterol; coronary artery disease; dysbetalipoproteinemia; atherosclerosis; myocardial infarction; stroke; embolus; angina; low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

EH	Key	Location/Qualifiers
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FT  modelled-size 1.18
/ note= "All Lys residues are Dimethyl-Lysine"
FT

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XX WO2004043403-A2.

XX 27-MAY-2004

13-NOV-2003: 2003WO-IIS036268-XX PF

XX  
PP 13-NOV-2003: 2002US-0425821PXX  
PA (IABR-) IABR RES FOUND

XX  
PT Anantharamiah GM. Garber DW. Datta G:

XX  
DB  
WPT: 2004-411629/38

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
PT  
PT comprises an amino acid sequence.

XX  
PS  
Claim 4: SEO ID NO 53: 79pp: English:

xx The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC containing the synthetic apolipoprotein-E mimicking polypeptide; a cell,  
 CC host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipemic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antitumoral. The synthetic apolipoprotein-E mimicking polypeptide is



CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX

SQ Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;  
Best Local Similarity 77.8%; Pred No. 1.8e-06;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRPIKAFYG 18

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Db 1 GIKRFLGSIWRPIKAFYG 18

Search completed: May 19, 2006, 14:24:31  
Job time : 95.2857 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds  
(without alignments)  
121.233 Million cell updates/sec

Title: US-10-712-447-116  
Perfect score: 98  
Sequence: 1 GLRRFIGSIWRFIRAFYQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80: \*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	49.0	627	2 S76462	hypothetical prote
2	47	48.0	516	2 T33269	hypothetical prote
3	45	45.9	489	2 B84733	probable cytochrom
4	44	44.9	246	2 I54412	MHC HLA-A cell sur
5	44	44.9	273	1 HLHU69	MHC class I histoc
6	44	44.9	365	1 HLHUA2	MHC class I histoc
7	44	44.9	365	2 I38443	Gene HLA-A-0203 pr
8	44	44.9	365	2 I61902	MHC class I histoc
9	44	44.9	365	2 I37542	MHC class I histoc
10	44	44.9	365	2 I84448	MHC class I histoc
11	44	44.9	365	2 I61857	MHC HLA-A2.4a chai
12	44	44.9	365	2 I38442	Gene HLA-A-0205 pr
13	44	44.9	589	2 A34341	poly(3-hydroxybuty
14	43	43.9	503	2 B81690	probable sodium-tr
15	43	43.9	519	1 T02263	cytochrome P450 DW
16	42.5	43.4	760	2 E84953	penicillin-binding
17	42	42.9	139	2 G64032	hypothetical prote
18	42	42.9	214	2 B72540	hypothetical prote
19	42	42.9	237	2 B72692	hypothetical prote
20	42	42.9	537	2 T04745	hypothetical prote
21	42	42.9	785	2 S63652	hypothetical prote
22	42	42.9	806	2 A84060	leucyl-tRNA synthet
23	42	42.9	861	2 H64102	leucine-tRNA ligas
24	42	42.9	1112	2 T42383	probable calcium-a
25	41.5	42.3	1025	2 AH3568	acridin resista
26	41	41.8	178	2 A75578	transcription regu
27	41	41.8	265	2 T32316	hypothetical prote
28	41	41.8	265	2 C42595	rfaP protein - Bac
29	41	41.8	359	2 T20575	hypothetical prote

ALIGNMENTS

RESULT 1

S76462  
hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID: A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;  
Best Local Similarity 38.9%; Pred. No. 8.2; Indels 0; Gaps 0;  
Matches 7; Conservative 6; Mismatches 5

Qy 1 GLRRFIGSIWRFIRAFYQ 18

Db 597 GLEQLLKKIWQLRQKFG 614

RESULT 2

T33269  
hypothetical protein C24B9.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T33269

R:Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid C24B9.

A:Reference number: 221310

A:Accession: T33269

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-516 <MUR>

A:Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1

A:Experimental source: strain Bristol N2; clone C24B9

C:Genetics:

A:Gene: CESP:C24B9.13

A:Map position: 5

A:Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 48.0%; Score 47; DB 2; Length 516;  
Best Local Similarity 52.9%; Pred. No. 9.8;



Nature 357, 326-329, 1992  
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
A;Reference number: 137120; MUID:92269955; PMID:1317015  
A;Accession: S77965  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-365 <BBL>  
A;Cross-references: UNIPARC:UPI0000124E24; EMBL:M84379; NID:G403143; PIDN:AAA59606.1; PII  
A;Experimental source: cell line GRC 138; isolate A\*0201  
R;Castano, A.R.; Lopez de Castro, J.A.  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992  
Immunogenetics 35, 344-346, 1992  
A;Title: Structure of the HLA-A\*0211 (A2.5) subtype: further evidence for selection-dri  
A;Reference number: S23593; MUID:92218010; PMID:1559719  
A;Accession: S23593  
A;Molecule type: mRNA  
A;Residues: 9-96, 'ID', 99-365 <CAS2>  
A;Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:G32156; PIDN:CAB56609.1; PID  
A;Note: this allele is designated A\*0211 (previously HLA-A2.5)  
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.  
Proc. Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979  
A;Title: Comparison of amino acid sequences of two human histocompatibility antigens, HL  
A;Reference number: A93834; MUID:80056745; PMID:92029  
A;Accession: A93834  
A;Molecule type: protein  
A;Residues: 25-55, 'Z', 57-60, 'B', 64-66, 'Z', 68-74, 'X', 76-85, 'RXXX', 90-94, 'AH', 97, 'V'  
A;Cross-references: UNIPARC:UPI00001737EE  
A;Note: this sequence has been revised in reference A93919  
R;Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.  
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982  
A;Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA-A2  
A;Reference number: A93919; MUID:82247941; PMID:6179086  
A;Accession: A93919  
A;Molecule type: protein  
A;Residues: 25-85, 'RXXX', 90-94, 'AH', 97, 'V', 99-112, 'Z', 114-118, 'LZ', 121-125, 'X', 127-131, '  
'232-265, 'E', 267-294 <LOP>  
A;Cross-references: UNIPARC:UPI00001737EF  
R;Silver, M.L.; Parker, K.C.; Wiley, D.C.  
Nature 350, 619-622, 1991  
A;Title: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-mic  
A;Reference number: S14802; MUID:91204056; PMID:2017257  
A;Accession: S14802  
A;Molecule type: protein  
A;Residues: 25-36 <SLI>  
A;Cross-references: UNIPARC:UPI00001737FO  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: 6p21.3-6p21.3  
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplanta  
F;1-24/DNA: signal sequence #status predicted <SIG>  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status expe  
F;25-114/DNA: alpha-1 <EX1>  
F;115-206/DNA: alpha-2 <EX2>  
F;120-285/DNA: immunoglobulin homology <IMM>  
F;307-331/DNA: transmembrane #status predicted <TM>  
F;332-365/DNA: intracellular #status predicted <INT>  
F;110/Binding site: carbohydrate (Aen) (covalent) #status experimental  
F;125-188, 227-283/Disulfide bonds: #status predicted

Query Match 44.9%; Score 44; DB 1; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 0; Gaps 0;  
QY 6 IGSWRFIRAFY 17  
DB 127 VGSDFRFLRGVH 138

RESULT 7  
138443

gene HLA-A-0203 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C;Accession: I38443  
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.  
J. Immunol. 139, 936-941, 1987  
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28  
A;Reference number: I38441; MUID:87252273; PMID:3496393  
A;Accession: I38443  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016A05E; EMBL:U03863; NID:G432438; PIDN:AAA03604.1; PII  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/DNA: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 6 IGSWRFIRAFY 17  
DB 127 VGSDFRFLRGVH 138

RESULT 8  
161902  
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A\*021  
C;Species: Homo sapiens (man)  
A;Variety: isolate A\*0212  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 23-Jul-1999  
C;Accession: I61902  
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I  
Nature 357, 326-329, 1992  
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
A;Reference number: I37120; MUID:92269955; PMID:1317015  
A;Accession: I61902  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AD39; GB:M84378; NID:G187625; PIDN:AAA59604.1; PID:5  
A;Experimental source: cell line KRC 033; isolate A\*0212  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: 6p21.3-6p21.3  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;1-24/DNA: signal sequence #status predicted <SIG>  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predic  
F;220-285/DNA: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 6 IGSWRFIRAFY 17  
DB 127 VGSDFRFLRGVH 138

RESULT 9  
137542  
MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A\*0216) precursor - hun  
C;Species: Homo sapiens (man)  
C;Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000  
C;Accession: I37542; S49582  
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.  
Immunogenetics 41, 388, 1995  
A;Title: Identification of a novel HLA-A2 subtype, HLA-A\*0216.  
A;Reference number: I37542; MUID:95278976; PMID:7759139  
A;Accession: I37542  
A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AA63; EMBL:Z46633; NID:9575248; PIDN:CAA86602.1; PID:  
A;Note: submitted to the EMBL Data Library, November 1994  
C;Genetics:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAFY 17  
: || ||| : :  
Db 127 VGSDWRFRLRGYH 138

RESULT 10  
I84448  
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A\*0211)  
A;Species: Homo sapiens (man)  
A;Variety: isolate A\*0211  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 23-Jul-1999  
C;Accession: I84448  
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;  
Nature 357, 326-329, 1992  
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
A;Reference number: I37120; MUID:92269955; PMID:1317015  
A;Accession: I84448  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:9187623; PIDN:AAA59603.1; PID:  
A;Experimental source: cell line GRC 138; isolate A\*0211  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: 9p21.3-9p21.3  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAFY 17  
: || ||| : :  
Db 127 VGSDWRFRLRGYH 138

RESULT 11  
I61857  
MHC HLA-A2.4a chain - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I61857  
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
J. Immunol. 142, 3937-3950, 1989  
A;Title: Diversity and diversification of HLA-A,B,C alleles.  
A;Reference number: I36956; MUID:89235215; PMID:2715640  
A;Accession: I61857  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AD48; GB:M24042; NID:9187777; PIDN:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;

Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAFY 17  
: || ||| : :  
Db 127 VGSDWRFRLRGYH 138

RESULT 12  
I38442  
Gene HLA-A-0205 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I38442  
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.  
J. Immunol. 139, 936-941, 1987  
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28  
A;Reference number: I38441; MUID:87252273; PMID:3496393  
A;Accession: I38442  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:9432436; PIDN:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAFY 17  
: || ||| : :  
Db 127 VGSDWRFRLRGYH 138

RESULT 13  
A34341  
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus  
C;Species: Alcaligenes eutrophus  
C;Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34341; A39190  
R;Peoples, O.P.; Sinskey, A.J.  
J. Biol. Chem. 264, 15298-15303, 1989  
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident  
A;Reference number: A34341; MUID:89359357; PMID:2670936  
A;Accession: A34341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-589 <PEO>  
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:9141958; PIDN:  
A;Experimental source: strain H16  
R;Schubert, P.; Krueger, N.; Steinbuechel, A.  
J. Bacteriol. 173, 168-175, 1991  
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt  
omoter.

Query Match 44.9%; Score 44; DB 2; Length 589;  
Best Local Similarity 47.6%; Pred. No. 34;  
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RRFPGSIW-----RPIAFY 17  
: || ||| : :  
Db 100 RRFAGDAWRTNLPYRFAAFY 120

```

Query Match      43.9%; Score 43; DB 2; Length 503;
Best Local Similarity 46.2%; Pred No. 42;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      2  LRFPGSIWRFIR 14
      |.:|.:|
Db      2  LEKFVDSLWKFRCR 14

```

RESULT 15  
T02263  
cytochrome P450 DWARF3 - maize  
N;Contains: oxidoreductase (EC 1.-.-.-)  
C;Species: Zea mays (maize)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T02263  
R;Winkler, R.G.; Helentjaris, T.  
Plant Cell 7, 1307-1317, 1995  
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberellin biosynthesis  
A;Reference number: Z14648; MUID:56004534; PMID:7549486  
A;Accession: T02263  
A;Status: preliminary; translated from GB/EMBL/DDBB  
A;Molecule type: mRNA  
A;Residues: 1-519 <WIN>  
A;Cross-reference: UNIPROT:Q43246; UNIPARC:UPI0000126CF8; EMBL:U32579; NID:G987266; PTD:G987266  
A;Experimental source: strain B73  
C;Genetics:  
A;Gene: dwarf3  
C;Function:  
A;Description: involved in an early step in gibberellin biosynthesis  
A;Pathway: gibberellin biosynthesis  
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology  
C;Keywords: oxidoreductase  
F:325-488/Domain: cytochrome P450 homology <P45>

Query Match	43.9%	Score 43;	DB 1;	Length 519;
Best Local Similarity	54.5%	Pred. NO. 43;		
Matches	6;	Conservative	3; Mismatches	2; Indels
				0; Gaps
Qy	6	IGSIWRTIRAF	16	
Db	82	VGGNWAFLRAF	92	

Search completed: May 19, 2006, 14:39:58  
Job time : 15.2857 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds  
(without alignments)  
144.247 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFIGSIWRIFAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	55.1	670	Q25271 LEPDE	Q25271 Leptinotars
2	54	55.1	805	Q3APY5_CHLCH	Q3APY5 chlorobium
3	51	52.0	488	Q84ZW1_PEA	Q84ZW1 pisum sativ
4	50	51.0	735	Q2F7V7_RHILV	Q2F7V7 rhizobium 1
5	48	49.0	361	Q2NDB5_SODGL	Q2NDB5 sodalis glo
6	48	49.0	401	Q2NKB3_GLOVI	Q2NKB3 gloebacter
7	48	49.0	449	Q3PK79_PARDE	Q3PK79 paracoccus
8	48	49.0	579	1 XKR7_HUMAN	Q5gh72 homo sapien
9	48	49.0	579	1 XKR7_PANTR	Q491s1 pan troglod
10	48	49.0	580	1 XKR7_MOUSE	Q5gh64 mus musculu
11	48	49.0	580	1 XKR7_RAT	Q5gh56 rattus norv
12	48	49.0	597	2 Q5AUS5_EMENI	Q5aus5 aspergillus
13	48	49.0	627	2 P74489_SYNY3	P74489 synchocyst
14	48	49.0	805	2 Q44QD1_CHILLI	Q44qd1 chlorobium
15	48	49.0	815	2 Q43K01_9CHLB	Q43k01 chlorobium
16	47	48.0	219	2 Q6L1V5_PICTO	Q6l1t5 picrophilus
17	47	48.0	287	2 Q76442_CABEL	Q76442 caenorhabdi
18	47	48.0	407	2 Q39L57_BURS3	Q39l57 burkholderi
19	47	48.0	408	2 Q456F4_9BURK	Q456f4 burkholderi
20	47	48.0	408	2 Q4LK44_9BURK	Q4lk44 burkholderi
21	47	48.0	486	2 Q5U414_YENLA	Q5u4i4 xenopus lae
22	47	48.0	487	2 Q32N49_YENLA	Q32n49 xenopus lae
23	47	48.0	506	2 Q5VRM7_ORISA	Q5vrm7 oryza sativ
24	47	48.0	607	2 Q425W5_DESHA	Q425w5 desulfitoba
25	46	46.9	426	2 Q99A07_9VIRU	Q99a07 torque teno
26	46	46.9	578	1 XKR6_TETNG	Q491s8 tetraodon n
27	46	46.9	578	2 Q5GH49_FUGRU	Q5gh49 fugu rubrip
28	46	46.9	836	2 Q2Y8V4_NITMU	Q2y8v4 nitrosospir
29	45	45.9	278	2 Q7VW93_BORPE	Q7vw93 bordetella
30	45	45.9	278	2 Q7W7P3_BORPA	Q7w7p3 bordetella
31	45	45.9	278	2 Q7WL31_BORBR	Q7wl31 bordetella

32 45 45.9 376 2 Q8KBA7\_CHLTE  
33 45 45.9 409 2 Q56YS1\_ARATH  
34 45 45.9 409 2 Q4BFM2\_BURVI  
35 45 45.9 435 2 Q2JIT0\_9CVAN  
36 45 45.9 458 2 Q3M6C5\_ANAVT  
37 45 45.9 458 2 Q8XG08\_RALSO  
38 45 45.9 489 1 KAO2\_ARATH  
39 45 45.9 490 2 Q84ZW0\_PEA  
40 45 45.9 513 2 Q00857\_FUSSP  
41 45 45.9 519 2 Q9C1B7\_FUSSP  
42 45 45.9 540 2 Q5GH65\_MOUSE  
43 45 45.9 580 2 Q5GH40\_BRARE  
44 45 45.9 638 1 XKR6\_RAT  
45 45 45.9 641 1 XKR6\_HUMAN

Q8kba7 chlorobium  
Q56ys1 arabidopsis  
Q4bfm2 burkholderi  
Q2jit0 cyanobacter  
Q3m6c5 anabaena va  
Q8xg08 ralstonia s  
Q8c5y2 arabidopsis  
Q84zw0 pisum sativ  
Q00857 fusarium sp  
Q9c1b7 fusarium sp  
Q5gh65 mus musculu  
Q5gh40 brachydanio  
Q5gh57 rattus norv  
Q5gh73 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q25271 LEPDE  
ID Q25271 LEPDE PRELIMINARY; PRT; 670 AA.  
AC Q25271; LEPDE  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE Diapause protein 1 (Fragment).  
GN Name=Dp19;  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;  
OC Leptinotarsa.  
OX NCBI\_TaxID=7539;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA de Kort C.A.D., Koopmanschap A.B.;  
RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding  
RT diapause protein 1, an amylphorin-type storage hexamer of the Colorado  
RT potato beetle."  
RL J. Insect Physiol. 40:527-535(1994).

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CC EMBL; X76080; CAA53691.1; -; mRNA.  
DR HSP; P04253; ILLI.  
DR GO; GO:0005344; F:oxygen transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000896; Hemocyanin.  
DR InterPro; IPR005203; hemocyanin C.  
DR InterPro; IPR005204; hemocyanin N.  
DR PANTHER; PTHR11511; Hemocyanin; 1.  
DR Pfam; PF03723; Hemocyanin\_C; 1.  
DR Pfam; PF00372; Hemocyanin\_M; 1.  
DR Pfam; PF03722; Hemocyanin\_N; 1.  
DR PRINTS; PR00187; HAEMOCYANIN.  
DR PROSITE; PS00210; HEMOCYANIN\_2; UNKNOWN\_1.  
FT NON TER 1  
SQ SEQUENCE 670 AA; 79825 MW; 8A000BA15BEC8A6 CRC64;

Query Match 55.1%; Score 54; DB 2; Length 670;

Best Local Similarity 43.8%; Pred. No. 9.8;

Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFIGSIWRIFAFVG 18

||| ||| ||| ||| ||| ||| |||

Db 351 RKFYGALWSYLRHFFG 366

##### RESULT 2

Q3APY5\_CHLCH  
ID Q3APY5\_CHLCH PRELIMINARY; PRT; 805 AA.

DR	GO: 0006118; P-electron transport; IEA.
DR	InterPro; IPR001128; Cytochrome_P450.
DR	InterPro; IPR002401; EP450I.
DR	PANTHER; PTHR19383; Cytochrome_P450; 1.
DR	Pfam; PF00067; P450; 2.
DR	PRINTS; PR00463; EP450I.
DR	PRINTS; PR00385; P450.
DR	PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW	Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW	Monooxygenase; Oxidoreductase.
SQ	SEQUENCE 488 AA; 56478 MW; 503453CB6E43C930 CRC64;
<p>Query Match 52.0%; Score 51; DB 2; Length 488;</p> <p>Best Local Similarity 66.7%; Pred. No. 21;</p> <p>Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps</p>	
QY	5 FTGSIWRFLRAF 16
DB	: :
	54 FIGNMWSFLRAF 65
RESULT 4	
Q9F7V7	RHLV PRELIMINARY; PRT; 735 AA.
AC	Q9F7V7;
DT	01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT	01-MAR-2001, sequence version 1.
DT	07-FEB-2006, entry version 25.
DE	ABC transporter RzcB.
GN	Names=rzcb;
OS	Rhizobium leguminosarum bv. viciae.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC	Rhizobiaceae; Rhizobium.
OX	NCBI_TaxID=387;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=305;
RX	MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjlm-47-6-495;
RT	Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
RA	"Analysis of the genetic region encoding a novel rhizobioicin from
RL	Rhizobium leguminosarum bv. viciae strain 305.";
RL	Can. J. Microbiol. 47:495-502(2001).
CC	-----
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
EMBL	AF273216; AAG25076.1; -; Genomic_DNA.
DR	HSSP; P08716; LMT0.
DR	GO: 0016021; C:integral to membrane; IEA.
DR	GO: 0005524; F:ATP binding; IEA.
DR	GO: 0016987; F:ATPase activity; IEA.
DR	GO: 0042626; F:ATPase activity, coupled to transmembrane m. .; IEA
DR	GO: 0000166; F:nucleotide binding; IEA.
DR	GO: 0008233; F:peptidase activity; IEA.
DR	GO: 0008565; F:protein transporter activity; IEA.
DR	GO: 0015031; P:protein transport; IEA.
DR	GO: 0006508; P:proteolysis; IEA.
DR	InterPro; IPR003593; AAA_ATPase.
DR	InterPro; IPR011527; ABC_TM_1.
DR	InterPro; IPR001140; ABC_TM_transp.
DR	InterPro; IPR003439; ABC_transp.like.
DR	InterPro; IPR005074; Peptidase_C39.
DR	InterPro; IPR010132; Type_I_sec_HlyB.
DR	PANTHER; PTHR19242:SF74; Type_I_sec_HlyB; 1.
DR	Pfam; PF00664; ABC_membrane; 1.
DR	Pfam; PF00005; ABC_tran; 1.
DR	Pfam; PF03412; Peptidase_C39; 1.
DR	ProDom; PD000006; ABC_transporter; 1.
DR	SMART; SM00382; AAA; 1.
DR	TIGRfams; TIGR01846; type_I_sec_HlyB; 1.
DR	PROSITE; PS50929; ABC_TMIF; 1.
DR	PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR	PROSITE; PS50993; ABC_TRANSPORTER_2; 1.

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DR PROSITE; PS50990; PEPTIDASE C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 51.0%; Score 50; DB 2; Length 735;
Best Local Similarity 56.2%; Pred. No. 47;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAF 16
DB 161 GFRWFLPALWRYRRAF 176

RESULT 5
ID Q2NUB5_SODGL PRELIMINARY; PRT; 361 AA.
AC Q2NUB5;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Putative glycosyltransferase.
GN ORFNames=SG0985;
OS Sodalitis glossinidius str. 'morsitans'.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalitis.
OX NCBI_TaxID=343509;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Morsitans;
RA Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RT "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalitis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156(2006).
CC
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CC
EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
DR Transferase.
SQ SEQUENCE 361 AA; 40347 MW; 1257F70F3C3CA6EC CRC64;

Query Match 49.0%; Score 48; DB 2; Length 361;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RFIGSIWRFIRAF 16
DB 62 RDVGSFWRFLSAF 74

RESULT 6
Q7NKW3_GLOVI
ID Q7NKW3_GLOVI PRELIMINARY; PRT; 401 AA.
AC Q7NKW3;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Gll1363 protein.
GN OrderedLocusNames=gll1363;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=335072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
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RL DNA Res. 10:137-145(2003).
CC
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CC
EMBL; BA000045; BAC89304.1; -; Genomic_DNA.
DR BioCyc; GVIO251221:GLU1363-MONOMER; -.
DR GO; GO:0004040; F:amidase activity; IEA.
DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3_hydro.
DR InterPro; IPR002901; Amidase_4.
DR Pfam; PF01520; Amidase_3; 1.
DR Pfam; PF01832; Glucosaminidase; 1.
KW Complete proteome.
SQ SEQUENCE 401 AA; 44051 MW; 903814BB688C170B CRC64;

Query Match 49.0%; Score 48; DB 2; Length 401;
Best Local Similarity 69.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFI 13
DB 104 GLERFIRGYWRFI 116

RESULT 7
Q3PK79_PARDE
ID Q3PK79_PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
GN ORFNames=PdenDRAFT_4722;
OS Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=318586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RA US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Paracoccus
RA denitrificans PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RA US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Paracoccus denitrificans
RA PD1222.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: Belongs to the cytochrome P450 family.
CC
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CC
EMBL; AA107000001; EAN68115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; p450; 1.
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DR PRINTS; PR00463; EP4501.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWNV.1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3BEC9E12AA3B35 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 449;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIWRFIRAF 16
Db 13 GSVWRIRDF 22

RESULT 8
XKR7 HUMAN
ID XKR7_HUMAN STANDARD; PRT; 579 AA.
AC Q5GH72; O9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=C20orf159, XRG7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark A., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslao M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -1- SIMILARITY. Belongs to the XK family.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
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CC EMBL; AY534245; AAT07094.1; -; mRNA.
DR EMBL; AU031658; CAB86102.1; ALT_SEQ; Genomic_DNA..
DR Ensembl; ENSG00000101321; Homo sapiens.
KW HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
FT CHAIN 1 579 XK-related protein 7.
FT /FTId=PRO_0000190788.
FT TRANSMEM 59 79 Potential.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 314 334 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF84B9EDD53D CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 9
XKR7_PANTR
ID XKR7_PANTR STANDARD; PRT; 579 AA.
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -1- SIMILARITY. Belongs to the XK family.
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CC EMBL; AY702910; AAV83783.1; -; mRNA.
KW Membrane; Transmembrane.
FT CHAIN 1 579 XK-related protein 7.
FT /FTId=PRO_0000190790.
FT TRANSMEM 59 79 Potential.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 314 334 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093E85D4 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

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RESULT 10
XKX7_MOUSE
ID_XKX7_MOUSE STANDARD; PRT; 580 AA.
AC Q5GH64;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP STRAIN=C57BL/6J;
RC Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC
CC -!- SIMILARITY: Belongs to the XK family.
CC -----
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CC -----
CC EMBL; AV534253; AAT07102.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
DR Membrane; Transmembrane.
KW CHAIN 1 580
FT FT TRANSMEM 59 79
FT FT TRANSMEM 89 109
FT FT TRANSMEM 260 280
FT FT TRANSMEM 303 323
FT FT TRANSMEM 326 346
FT FT TRANSMEM 355 375
FT FT TRANSMEM 384 404
FT FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64302 MW; F3291FABP4C5A826 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 580;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGSIWRFIRAFY 17
Db 190 LGQWRYLRALY 201
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RESULT 11
XKX7_RAT
ID_XKX7_RAT STANDARD; PRT; 580 AA.
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP STRAIN=Sprague-Dawley;
RC Huang C.-H., Chen Y.;

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RC	STRAIN=DSM 245;
RG	US DOE Joint Genome Institute (JGI-PGFI);
RH	Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RI	Hammann N., Israni S., Pitluck S., Richardson P.;
RA	"Sequencing of the draft genome and assembly of Chlorobium limicola
RT	DSM 245.";
RL	Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=DSM 245;
RG	US DOE Joint Genome Institute (JGI-ORNL);
RH	Larimer F., Land M.;
RI	"Annotation of the draft genome assembly of Chlorobium limicola DSM
RT	245.";
RL	Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN	CC -I- CAUTION: The sequence shown here is derived from an
RP	EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
RC	preliminary data.
RG	CC -----
RH	CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
RI	CC Distributed under the Creative Commons Attribution-NoDerivs License
RA	CC -----
RT	DR EMBL; AHJ01000009; EAM43320.1; -: Genomic_DNA.
RL	GO; GO:0005524; F:ATP binding; IEA.
RN	DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
RP	DR GO; GO:0006429; F:leucyl-tRNA aminoacylation; IEA.
RC	DR InterPro; IPR002302; Leu tRNAsyn_1a.
RG	DR Pfam; PF00133; tRNA-synt_1; 1.
RH	DR PRINTS; PR00985; TRNASYNTHLEU.
RI	DR TIGRFAMS; TIGR00396; leuS_bact; 1.
RT	KW Aminoacyl-tRNA synthetase.
RL	SQ SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
RN	Query Match 49.0%; Score 48; DB 2; Length 805;
RP	Best Local Similarity 46.2%; Pred.No 1.1e+02;
RC	Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNAasn_la.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFams; TIGR00396; leus_bact; 1.
KW Aminoacyl-tRNA synthetase
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 816;
Best Local Similarity 46.2%; Pred.No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFI 13
Db 622 GISRFLGKVRV 634
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Search completed: May 19, 2006, 14:38:14  
Job time : 116.429 secs

**This Page Blank (uspto)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds  
(without alignments)  
63.384 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFGSIWRIFAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pep:\*

2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pep:\*

3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pep:\*

4: /EMC Celerra\_SIDS3/ptodata/2/iaa/8 COMB.pep:\*

5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	75.5	18	2	US-08-940-095-242
2	74	75.5	18	2	US-08-940-093-242
3	74	75.5	18	2	US-08-940-096-242
4	74	75.5	18	2	US-09-465-719-242
5	74	75.5	18	2	US-09-453-605-242
6	74	75.5	18	2	US-09-453-838-242
7	74	75.5	18	2	US-08-940-136-242
8	74	75.5	18	2	US-09-453-841-242
9	74	75.5	18	2	US-09-453-833-242
10	74	75.5	18	2	US-09-453-826-242
11	74	75.5	18	2	US-09-453-840-242
12	74	75.5	18	2	US-09-865-989-242
13	74	75.5	18	2	US-09-453-834-242
14	74	75.5	18	2	US-10-283-599-242
15	74	75.5	18	2	US-09-465-718-242
16	50	51.0	76	2	US-09-205-258-892
17	50	51.0	76	2	US-10-004-860-892
18	44	44.9	14	1	US-08-480-190-3
19	44	44.9	14	1	US-08-488-379-3
20	44	44.9	14	2	US-08-475-399A-3
21	44	44.9	14	2	US-08-077-255A-3
22	44	44.9	14	5	PCT-US93-07545-3
23	44	44.9	15	1	US-08-480-190-2
24	44	44.9	15	1	US-08-488-379-2
25	44	44.9	15	2	US-08-475-399A-2
26	44	44.9	15	2	US-08-077-255A-2

27	44	44.9	15	5	PCT-US93-07545-2	Sequence 2, Appli
28	44	44.9	18	1	US-08-480-190-1	Sequence 1, Appli
29	44	44.9	18	1	US-08-480-190-61	Sequence 61, Appli
30	44	44.9	18	1	US-08-488-379-1	Sequence 1, Appli
31	44	44.9	18	1	US-08-488-379-61	Sequence 61, Appli
32	44	44.9	18	2	US-08-475-399A-1	Sequence 1, Appli
33	44	44.9	18	2	US-08-475-399A-61	Sequence 61, Appli
34	44	44.9	18	2	US-08-077-255A-1	Sequence 1, Appli
35	44	44.9	18	2	US-08-077-255A-61	Sequence 61, Appli
36	44	44.9	18	5	PCT-US93-07545-1	Sequence 1, Appli
37	44	44.9	18	5	PCT-US93-07545-61	Sequence 61, Appli
38	44	44.9	156	2	US-09-513-999C-4289	Sequence 4289, Ap
39	44	44.9	182	1	US-08-127-954-137	Sequence 137, App
40	44	44.9	182	1	US-08-127-954-138	Sequence 138, App
41	44	44.9	182	1	US-08-127-954-139	Sequence 139, App
42	44	44.9	182	1	US-08-127-954-140	Sequence 140, App
43	44	44.9	182	1	US-08-127-954-141	Sequence 141, App
44	44	44.9	182	1	US-08-127-954-142	Sequence 142, App
45	44	44.9	182	1	US-08-127-954-144	Sequence 144, App

ALIGNMENTS

RESULT 1  
US-08-940-095-242  
; Sequence 242, Application US/08940095  
; Patent No. 6004925  
; GENERAL INFORMATION:  
; APPLICANT: Daseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Butner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: ANTIPOPROTEIN A-I AGONISTS  
; TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDEMIC DISORDERS  
; NUMBER OF SEQUENCES: 258  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,095  
; FILING DATE: 29-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 009196-0004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 242:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6004925e  
US-08-940-095-242



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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIKAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
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; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIKAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
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US-09-453-838-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFTRAFVG 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFVG 18

## RESULT 7

US-08-940-136-242

; Sequence 242, Application US/08940136  
; Patent No. 6518412

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: GENE THERAPY APPROACHES TO

; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR

; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/940,136

; FILING DATE: 29-SEP-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0007-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6518412e

; US-08-940-136-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFTRAFVG 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFVG 18

## RESULT 8

US-09-453-841-242

; Sequence 242, Application US/09453841

; Patent No. 6573239

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/453,841

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/940,095

; FILING DATE: 29-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0004-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6573239e

; US-09-453-841-242

Query Match 75.5%; Score 74; DB 2; Length 18;

Best Local Similarity 61.1%; Pred. No. 3.9e-05;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFTRAFVG 18

|:::|:::|:::|:::|

Db 1 GIKKFLGSIWKFIKAFVG 18

## RESULT 9

US-09-453-833-242

; Sequence 242, Application US/09453833

; Patent No. 6602854

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,833  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6602854e  
US-09-453-833-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 10  
US-09-453-826-242  
Sequence 242, Application US/09453826  
Patent No. 6630450  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,826  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6630450e  
US-09-453-826-242  
Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 3.9e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GLRRFGSIWRFIRAFVG 18  
|:::|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFVG 18  
RESULT 11  
US-09-453-840-242  
Sequence 242, Application US/09453840  
Patent No. 6716816  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,840  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716a16e
US-09-453-840-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION:
; APPLICATION DATA:
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; APPLICATION DATA: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,599

FILING DATE: 29-OCT-2002

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,136

FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0007-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6844327e

US-10-283-599-242

Query Match 75.5%; Score 74; DB 2; Length 18;

Best Local Similarity 61.1%; Pred. No. 3.9e-05;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFIRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

Sequence 242, Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/465,718

FILING DATE: 17-Dec-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/940,096

FILING DATE: 29-SEP-1997

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6900177e

US-09-465-718-242

Query Match 75.5%; Score 74; DB 2; Length 18;

Best Local Similarity 61.1%; Pred. No. 3.9e-05;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFIRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55

Job time : 24.8571 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 seconds  
(without alignments)  
102.575 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98  
Sequence: 1 GLRRFGSIWRFFIRAFYG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US07\_PUBCOMB.psp.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US08\_PUBCOMB.psp.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US09\_PUBCOMB.psp.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US10A\_PUBCOMB.psp.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US10B\_PUBCOMB.psp.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubpaa/US11\_PUBCOMB.psp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	98	100.0	18	4	US-10-712-447-116
3	94	95.9	18	4	US-10-712-447-2
4	94	95.9	18	4	US-10-712-447-5
5	94	95.9	18	4	US-10-712-447-8
6	94	95.9	18	4	US-10-712-447-10
7	94	95.9	18	4	US-10-712-447-13
8	94	95.9	18	4	US-10-712-447-117
9	94	95.9	18	4	US-10-712-447-127
10	94	95.9	18	4	US-10-712-447-131
11	91	92.9	18	4	US-10-712-447-91
12	90	91.8	18	4	US-10-712-447-129
13	88	89.8	18	4	US-10-712-447-21
14	88	89.8	18	4	US-10-712-447-53
15	88	89.8	18	4	US-10-712-447-74
16	86	87.8	18	4	US-10-712-447-4
17	86	87.8	18	4	US-10-712-447-112
18	85	86.7	18	4	US-10-712-447-99
19	84	85.7	18	4	US-10-712-447-18
20	84	85.7	18	4	US-10-712-447-113
21	84	85.7	18	4	US-10-712-447-114
22	83	84.7	18	4	US-10-712-447-17
23	83	84.7	18	4	US-10-712-447-121
24	82	83.7	18	4	US-10-712-447-61
25	82	83.7	18	4	US-10-712-447-82
26	81	82.7	18	4	US-10-712-447-16
27	81	82.7	18	4	US-10-712-447-96

28	80	81.6	18	4	US-10-712-447-22	Sequence 22, Appl
29	80	81.6	18	4	US-10-712-447-78	Sequence 78, Appl
30	80	81.6	18	4	US-10-712-447-95	Sequence 95, Appl
31	80	81.6	18	4	US-10-712-447-120	Sequence 120, Appl
32	78	79.6	18	4	US-10-712-447-19	Sequence 19, Appl
33	78	79.6	18	4	US-10-712-447-56	Sequence 56, Appl
34	78	79.6	18	4	US-10-712-447-58	Sequence 58, Appl
35	78	79.6	18	4	US-10-712-447-77	Sequence 77, Appl
36	78	79.6	18	4	US-10-712-447-79	Sequence 79, Appl
37	78	79.6	18	4	US-10-712-447-80	Sequence 80, Appl
38	78	79.6	18	4	US-10-712-447-94	Sequence 94, Appl
39	77	78.6	18	4	US-10-712-447-57	Sequence 57, Appl
40	77	78.6	18	4	US-10-712-447-100	Sequence 100, Appl
41	76	77.6	18	4	US-10-712-447-41	Sequence 41, Appl
42	76	77.6	18	4	US-10-712-447-119	Sequence 119, Appl
43	75	76.5	18	4	US-10-712-447-97	Sequence 97, Appl
44	74	75.5	18	3	US-09-865-989-242	Sequence 242, Appl
45	74	75.5	18	3	US-09-865-989-242	Sequence 242, Appl

#### ALIGNMENTS

RESULT 1  
US-10-712-447-115  
; Sequence 115, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 115  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION:  
US-10-712-447-115

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFFIRAFYG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GLRRFGSIWRFFIRAFYG 18

RESULT 2  
US-10-712-447-116  
; Sequence 116, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10/712,447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13

1

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RESULT 10
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131

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Job time : 81.2857 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds  
(without alignments)  
17.943 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFIGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pbp.\*
- 2: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pbp.\*
- 3: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pbp.\*
- 4: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pbp.\*
- 5: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pbp.\*
- 6: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pbp.\*
- 7: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pbp.\*
- 8: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	38.8	74	1	US-09-949-925-111
2	37.5	38.3	441	6	US-10-511-937-2947
3	35	35.7	651	6	US-10-511-937-2401
4	34.5	35.2	60	1	US-09-949-925-142
5	34	34.7	522	6	US-10-505-928-543
6	34	34.7	599	7	US-11-302-678-5
7	33.5	34.2	244	7	US-11-169-140-109
8	33.5	34.2	503	7	US-11-024-544A-21
9	33.5	34.2	503	7	US-11-190-750-135
10	33.5	34.2	503	7	US-11-264-784-87
11	33	33.7	313	7	US-11-242-505A-48
12	33	33.7	342	7	US-11-204-427-7
13	33	33.7	393	7	US-11-304-129-40
14	33	33.7	403	7	US-11-304-129-48
15	33	33.7	403	7	US-11-242-505A-18
16	33	33.7	463	6	US-10-505-928-545
17	33	33.7	643	6	US-10-504-120-19
18	33	33.7	667	7	US-11-311-555-16
19	33	33.7	667	7	US-11-311-561-16
20	33	33.7	714	6	US-10-868-498-2
21	33	33.7	919	7	US-11-302-678-62
22	32	32.7	351	6	US-10-511-937-2540
23	32	32.7	364	7	US-11-113-081A-6
24	32	32.7	388	6	US-10-196-749-336
25	32	32.7	388	7	US-11-024-544A-169

26	32	32.7	388	7	US-11-190-750-137
27	32	32.7	388	7	US-11-204-427-1
28	32	32.7	423	7	US-11-312-958-12
29	32	32.7	464	6	US-10-488-015-17
30	32	32.7	544	6	US-10-505-928-859
31	32	32.7	627	7	US-11-249-111-88
32	32	32.7	747	7	US-11-261-384-2
33	32	32.7	764	7	US-11-223-738-6
34	31.5	32.1	4590	6	US-10-505-928-569
35	31	31.6	126	7	US-11-075-891-23
36	31	31.6	166	7	US-11-280-997-1
37	31	31.6	166	7	US-11-280-997-2
38	31	31.6	166	7	US-11-280-997-3
39	31	31.6	166	7	US-11-280-997-23
40	31	31.6	166	7	US-11-280-997-24
41	31	31.6	166	7	US-11-280-997-25
42	31	31.6	166	7	US-11-280-997-26
43	31	31.6	187	7	US-11-183-218-6
44	31	31.6	581	7	US-11-251-465-18
45	31	31.6	630	7	US-11-146-700-3

#### ALIGNMENTS

##### RESULT 1

US-09-949-925-111  
; Sequence 111, Application US/09949925  
; Publication No. US2006009575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (74)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-949-925-111

Query Match 38.8%; Score 38; DB 1; Length 74;  
Best Local Similarity 63.6%; Pred. No. 1.1;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LRRFIGSIWRF 12

|||||





; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 543  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;  
Best Local Similarity 47.1%; Pred. No. 55;  
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 3 RRPI-GSIWRFTRAFY 17  
Db 473 RRFTQGDLYRHIRKHF 489  
||| |::| |::| |::| |::|

RESULT 6  
US-11-302-678-5  
; Sequence 5, Application US/11302678  
; Publication No. US20060088881A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012P1RNM OMNI  
; CURRENT APPLICATION NUMBER: US/11/302,678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-302-678-5

Query Match 34.7%; Score 34; DB 7; Length 599;  
Best Local Similarity 57.1%; Pred. No. 64;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IGSIWRF 12  
Db 64 LGNVWRF 70  
:|::| |::| |::| |::|

RESULT 7  
US-11-169-140-109

; Sequence 109, Application US/11169140  
; Publication No. US20060099150A1  
; GENERAL INFORMATION:  
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou L.  
; APPLICANT: SHERIDAN, Philip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven  
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CSI  
; TITLE OF INVENTION: BARRIERS  
; FILE REFERENCE: 11474-037-999  
; CURRENT APPLICATION NUMBER: US/11/169,140  
; CURRENT FILING DATE: 2005-06-27  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/949,039  
; PRIOR FILING DATE: 2001-09-06  
; PRIOR APPLICATION NUMBER: 09/969,748  
; PRIOR FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 109  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Simian  
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;  
Best Local Similarity 42.1%; Pred. No. 27;  
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

Qy 1 GLRRFIGSIW-----RFR 14  
Db 158 GLVLALGAVCVARAFIR 176  
|| |::| |::| |::| |::|

RESULT 8  
US-11-024-544A-21  
; Sequence 21, Application US/11024544A  
; Publication No. US20060094086A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
; APPLICANT: Yadav, Narendra  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Zhang, Hongxiang  
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED  
; TITLE OF INVENTION: FATTY ACIDS AND OIL CONTENT IN OLEAGINOUS ORGANISMS  
; FILE REFERENCE: CL2717  
; CURRENT APPLICATION NUMBER: US/11/024,544A  
; CURRENT FILING DATE: 2004-12-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea 70-15  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank Accession No. EAA52634  
; DATABASE ENTRY DATE: 2003-10-31  
; RELEVANT RESIDUES: (1)..(503)  
US-11-024-544A-21

Query Match 34.2%; Score 33.5; DB 7; Length 503;  
Best Local Similarity 43.8%; Pred. No. 64;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18  
|||: ||: |  
Db 156 RRFV-STWKLIALVHG 170

RESULT 9  
US-11-190-750-135  
; Sequence 135, Application US/11190750  
; Publication No. US20060094089A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Yadav, Narendra  
; APPLICANT: Zhang, Hongxiang  
; TITLE OF INVENTION: ACYTRANSFERRASE REGULATION TO INCREASE THE PERCENT OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF  
; TITLE OF INVENTION: OLEAGINOUS ORGANISMS  
; FILE REFERENCE: CL2718  
; CURRENT APPLICATION NUMBER: US/11/190,750  
; CURRENT FILING DATE: 2005-07-27  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 135  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]  
US-11-190-750-135

Query Match 34.2%; Score 33.5; DB 7; Length 503;  
Best Local Similarity 43.8%; Pred. No. 64;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18  
|||: ||: |  
Db 156 RRFV-STWKLIALVHG 170

RESULT 10  
US-11-264-784-87  
; Sequence 87, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gallies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 87  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: DGAT1  
US-11-264-784-87

Query Match 34.2%; Score 33.5; DB 7; Length 503;  
Best Local Similarity 43.8%; Pred. No. 64;  
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18

Db 156 RRFV-STWKLIALVHG 170  
|||: ||: |  
|||: ||: |

RESULT 11  
US-11-242-505A-48  
; Sequence 48, Application US/11242505A  
; Publication No. US20060099656A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Healy, Aileen  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 13848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, 5  
; FILE REFERENCE: MPI2001-288P1RCPIOMNIM  
; CURRENT APPLICATION NUMBER: US/11/242,505A  
; CURRENT FILING DATE: 2005-10-03  
; PRIOR APPLICATION NUMBER: US 10/290,078  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 60/347,949  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: US 10/320,351  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,606  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-242-505A-48

Query Match 33.7%; Score 33; DB 7; Length 313;  
Best Local Similarity 62.5%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 WRFIRAFY 17  
|||: ||: |  
Db 199 WSFLDAFY 206

RESULT 12  
US-11-204-427-7  
; Sequence 7, Application US/11204427  
; Publication No. US20060100146A1  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L  
; APPLICANT: Turkish, Aaron R  
; APPLICANT: Billheimer, Jeffrey T  
; APPLICANT: Cromley, Debra  
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES  
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS  
; CURRENT APPLICATION NUMBER: US/11/204,427  
; CURRENT FILING DATE: 2005-08-15  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;  
Best Local Similarity 50.0%; Pred. No. 50;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SWRFIRAFY 17  
|||: ||: |  
Db 84 AIWRQRDIY 93

RESULT 13

US-11-304-129-40  
 ; Sequence 40, Application US/11304129  
 ; Publication No. US20060088915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OHTAKI, Tetsuya  
 ; APPLICANT: MASUDA, Yasushi  
 ; APPLICANT: TAKATSU, Yoshihiro  
 ; APPLICANT: WATANABE, Takuya  
 ; APPLICANT: TERAQ, Yasuko  
 ; APPLICANT: SHINTANI, Yasushi  
 ; APPLICANT: HINUMA, Syuji  
 ; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
 ; FILE REFERENCE: 2762USOP  
 ; CURRENT APPLICATION NUMBER: US/11/304,129  
 ; CURRENT FILING DATE: 2005-12-15  
 ; PRIOR APPLICATION NUMBER: US/10/333,192  
 ; PRIOR FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: JP 2000-217442  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: JP 2001-26779  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
 ; PRIOR FILING DATE: 2001-07-17  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SEQ ID NO 40  
 ; LENGTH: 393  
 ; TYPE: PRT  
 ; ORGANISM: Rat  
 ; US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;  
 Best Local Similarity 46.2%; Pred. No. 58;  
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FIGSIWRFIRAFY 17  
 ||||| : ||  
 Db 216 FCGIWPVDQIFY 228

RESULT 14  
 US-11-304-129-48  
 ; Sequence 48, Application US/11304129  
 ; Publication No. US20060088915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OHTAKI, Tetsuya  
 ; APPLICANT: MASUDA, Yasushi  
 ; APPLICANT: TAKATSU, Yoshihiro  
 ; APPLICANT: WATANABE, Takuya  
 ; APPLICANT: TERAQ, Yasuko  
 ; APPLICANT: SHINTANI, Yasushi  
 ; APPLICANT: HINUMA, Syuji  
 ; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof  
 ; FILE REFERENCE: 2762USOP  
 ; CURRENT APPLICATION NUMBER: US/11/304,129  
 ; CURRENT FILING DATE: 2005-12-15  
 ; PRIOR APPLICATION NUMBER: US/10/333,192  
 ; PRIOR FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: JP 2000-217442  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: JP 2001-26779  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06162  
 ; PRIOR FILING DATE: 2001-07-17  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SEQ ID NO 48  
 ; LENGTH: 393  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 ; US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;  
 Best Local Similarity 46.2%; Pred. No. 58;  
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FIGSIWRFIRAFY 17  
 ||||| : ||  
 Db 216 FCGIWPVDQIFY 228

RESULT 15  
 US-11-242-505A-18  
 ; Sequence 18, Application US/11242505A  
 ; Publication No. US20060099656A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carroll, Joseph M.  
 ; APPLICANT: Healy, Aileen  
 ; TITLE OF INVENTION: Methods and Compositions for Treating  
 ; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
 ; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,  
 ; FILE REFERENCE: MPI2001-288P1RCP10NMIM  
 ; CURRENT APPLICATION NUMBER: US/11/242,505A  
 ; CURRENT FILING DATE: 2005-10-03  
 ; PRIOR APPLICATION NUMBER: US 10/290,078  
 ; PRIOR FILING DATE: 2002-11-07  
 ; PRIOR APPLICATION NUMBER: US 60/347,949  
 ; PRIOR FILING DATE: 2001-11-07  
 ; PRIOR APPLICATION NUMBER: US 10/320,351  
 ; PRIOR FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: 60/341,606  
 ; PRIOR FILING DATE: 2001-12-17  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 18  
 ; LENGTH: 403  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; US-11-242-505A-18

Query Match 33.7%; Score 33; DB 7; Length 403;  
 Best Local Similarity 44.4%; Pred. No. 60;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LRRFIGSIW 10  
 :||| :|||  
 Db 155 VRRVLGAVW 163

Search completed: May 19, 2006, 15:28:18  
 Job time : 3.14286 secs

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OM protein - protein search, using sw model  
Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds  
(without alignments)  
87.287 Million cell updates/sec

Title: US-10-712-447-117  
Perfect score: 98  
Sequence: 1 GIRFIGSIWFLRAFG 18  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2589679 seqs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 8:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*
- 10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	98	100.0	18	ADO34340	Ado34340 Synthetic
2	94	95.9	18	ADO34231	Ado34231 Synthetic
3	94	95.9	18	ADO34354	Ado34354 Synthetic
4	94	95.9	18	ADO34225	Ado34225 Synthetic
5	94	95.9	18	ADO34338	Ado34338 Synthetic
6	94	95.9	18	ADO34352	Ado34352 Synthetic
7	94	95.9	18	ADO34228	Ado34228 Synthetic
8	94	95.9	18	ADO34236	Ado34236 Synthetic
9	94	95.9	18	ADO34339	Ado34339 Synthetic
10	94	95.9	18	ADO34233	Ado34233 Synthetic
11	94	95.9	18	ADO34350	Ado34350 Synthetic
12	91	92.9	18	ADO34314	Ado34314 Synthetic
13	88	89.8	18	ADO34297	Ado34297 Synthetic
14	88	89.8	18	ADO34244	Ado34244 Synthetic
15	88	89.8	18	ADO34276	Ado34276 Synthetic
16	86	87.8	18	ADO34336	Ado34336 Synthetic
17	86	87.8	18	ADO34227	Ado34227 Synthetic
18	85	86.7	18	ADO34322	Ado34322 Synthetic
19	84	85.7	18	ADO34335	Ado34335 Synthetic
20	84	85.7	18	ADO34337	Ado34337 Synthetic
21	84	85.7	18	ADO34241	Ado34241 Synthetic
22	83	84.7	18	ADO34240	Ado34240 Synthetic
23	83	84.7	18	ADO34344	Ado34344 Synthetic

24	82	83.7	18	8	ADO34284	Ado34284 Synthetic
25	82	83.7	18	8	ADO34305	Ado34305 Synthetic
26	81	82.7	18	8	ADO34239	Ado34239 Synthetic
27	81	82.7	18	8	ADO34319	Ado34319 Synthetic
28	80	81.6	18	8	ADO34245	Ado34245 Synthetic
29	80	81.6	18	8	ADO34301	Ado34301 Synthetic
30	80	81.6	18	8	ADO34343	Ado34343 Synthetic
31	80	81.6	18	8	ADO34318	Ado34318 Synthetic
32	78	79.6	18	8	ADO34302	Ado34302 Synthetic
33	78	79.6	18	8	ADO34279	Ado34279 Synthetic
34	78	79.6	18	8	ADO34303	Ado34303 Synthetic
35	78	79.6	18	8	ADO34242	Ado34242 Synthetic
36	78	79.6	18	8	ADO34300	Ado34300 Synthetic
37	78	79.6	18	8	ADO34281	Ado34281 Synthetic
38	78	79.6	18	8	ADO34317	Ado34317 Synthetic
39	77	78.6	18	8	ADO34323	Ado34323 Synthetic
40	77	78.6	18	8	ADO34280	Ado34280 Synthetic
41	76	77.6	18	8	ADO34341	Ado34341 Synthetic
42	76	77.6	18	8	ADO34333	Ado34333 Synthetic
43	76	77.6	18	8	ADO34264	Ado34264 Synthetic
44	75	76.5	18	8	ADO34320	Ado34320 Synthetic
45	74	75.5	18	2	AA18917	Aay18917 Lecithin:

ALIGNMENTS

RESULT 1  
ADO34340  
ID ADO34340 standard; peptide; 18 AA.  
XX  
AC ADO34340;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 117.  
XX  
KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiactant;  
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
XX  
OS Synthetic.  
XX  
PN WO2004043403-A2.  
XX  
PD 27-MAY-2004.  
XX  
PF 13-NOV-2003; 2003WO-US036268.  
XX  
PR 13-NOV-2002; 2002US-0425821P.  
XX  
FA (UABR-) UAB RES FOUND.  
XX  
PI Anantharamiah GM, Garber DW, Datta G;  
XX  
DR WPI; 2004-411629/38.  
XX  
DR Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
comprises an amino acid sequence.  
XX  
PT  
XX  
PS Claim 4; SEQ ID NO 117; 79pp; English.  
XX  
CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
polypeptide. The invention further comprises an isolated nucleic acid  
encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
a host cell, a recombinant cell or a transgenic, non-human subject  
(including animal or plant) comprising the synthetic apolipoprotein-E  
mimicking polypeptide encoding polynucleotide; a composition comprising  
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFLRAFYG 18  
 |||||:|||||:|||||  
 Db 1 GIRRFIGSIWRFLRAFYG 18

## RESULT 2

ADO34231  
 ID ADO34231 standard; peptide; 18 AA.

AC ADO34231;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFLRAFYG 18  
 |||||:|||||:|||||  
 Db 1 GIRRFIGSIWRFLRAFYG 18

## RESULT 3

ADO34354

ID ADO34354 standard; peptide; 18 AA.

AC ADO34354;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 131; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFIGSIWRFLRAFYG 18  
 | : | | : | | | | | | | | | |  
 Db 1 GLRFLGSIWRFLRAFYG 18

RESULT 4  
 ADO34225  
 ID ADO34225 standard; peptide; 18 AA.

AC ADO34225;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 18 /note= "C-terminal amide"

FT WO2004043403-A2.

PN 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 2; 79pp; English.

CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFIGSIWRFLRAFYG 18  
 | : | | : | | | | | | | | | |  
 Db 1 GRRFLGSIWRFLRAFYG 18

RESULT 5  
 ADO34338  
 ID ADO34338 standard; peptide; 18 AA.

XX ADO34338;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

PN WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 115; 79pp; English.

CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFLRAFYG 18  
 |:|||||||:|||||  
 Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 6  
 ADO34352  
 ID ADO34352 standard; peptide; 18 AA.

XX  
 AC ADO34352;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 129.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 129; 79pp; English.

XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFLRAFYG 18  
 |:|||||||:|||||  
 Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 7  
 ADO34228  
 ID ADO34228 standard; peptide; 18 AA.

XX  
 AC ADO34228;

XX  
 DT 12-AUG-2004 (first entry)

XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 5.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX  
 OS Synthetic.

XX  
 PN WO2004043403-A2.

XX  
 PD 27-MAY-2004.

XX  
 PF 13-NOV-2003; 2003WO-US036268.

XX  
 PR 13-NOV-2002; 2002US-0425821P.

XX  
 PA (UABR-) UAB RES FOUND.

XX  
 PI Anantharamiah GM, Garber DW, Datta G;

XX  
 DR WPI; 2004-411629/38.

XX  
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX  
 PS Claim 4; SEQ ID NO 5; 79pp; English.

XX  
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic



CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX  
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGIWRFLRAFYG 18  
 |||||:|||||:|||||  
 Db 1 GIRRFLGSIWRFLRAFYG 18

RESULT 8  
 ADO34236  
 ID ADO34236 standard; peptide; 18 AA.

XX  
 AC ADO34236;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.  
 XX  
 OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGIWRFLRAFYG 18  
 |||||:|||||:|||||  
 Db 1 GIRRFLGSIWRFLRAFYG 18

RESULT 9  
 ADO34339  
 ID ADO34339 standard; peptide; 18 AA.

XX ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFTGSIWRFLRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFTGSIWRFLRAFYG 18

RESULT 10

ADO34233  
 ID ADO34233 standard; peptide; 18 AA.

XX AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GW, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFTGSIWRFLRAFYG 18  
 |:|||||:|||||  
 Db 1 GLRRFTGSIWRFLRAFYG 18

RESULT 11

ADO34350  
 ID ADO34350 standard; peptide; 18 AA.

XX AC ADO34350;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 127.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GW, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 127; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.6e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFGISLWRFRAFYG 18

|:|||||:|||||

Db 1 GLRRFGISLWRFRAFYG 18

RESULT 12

ADO34314

ID ADO34314 standard; peptide; 18 AA.

XX AC ADO34314;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

XX KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;

XX KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;

XX KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

XX KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating

XX PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis

XX PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 91; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking

XX CC polypeptide. The invention further comprises an isolated nucleic acid

XX CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

XX CC a host cell, a recombinant cell or a transgenic, non-human subject

XX CC (including animal or plant) comprising the synthetic apolipoprotein-E

XX CC mimicking polypeptide encoding polynucleotide; a composition comprising

XX CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

XX CC an monoclonal antibody that specifically binds to the synthetic

XX CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

XX CC mimicking polypeptide has the following activities: antilipaeamic,

XX CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

XX CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

XX CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 92.9%; Score 91; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 4.8e-07;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFGISLWRFRAFYG 18

|||:|:|||||:|||||

Db 1 GRRFGISLWRFRAFYG 18

RESULT 13

ADO34297

ID ADO34297 standard; peptide; 18 AA.

XX AC ADO34297;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 74.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

XX KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;

XX KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;

XX KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

XX KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating

XX PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis

XX PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 74; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking

XX CC polypeptide. The invention further comprises an isolated nucleic acid

XX CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

XX CC a host cell, a recombinant cell or a transgenic, non-human subject

XX CC (including animal or plant) comprising the synthetic apolipoprotein-E

XX CC mimicking polypeptide encoding polynucleotide; a composition comprising

XX CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

XX CC an monoclonal antibody that specifically binds to the synthetic

XX CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

XX CC mimicking polypeptide has the following activities: antilipaeamic,

XX CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

XX CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

XX CC useful for reducing serum cholesterol in a subject (including a mammal

XX CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,  
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;  
 Best Local Similarity 77.8%; Pred. No. 1.4e-06;  
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFSGIWRFLRFAYG 18  
 ||||:|||||:||||  
 Db 1 GIRKFLGSIWRFIKAFYG 18

RESULT 14  
 ADO34244  
 ID ADO34244 standard; peptide; 18 AA.

XX ADO34244;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 21; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,

CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
 CC myocardial infarction or stroke; for breaking an embolus in the subject;  
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;  
 Best Local Similarity 77.8%; Pred. No. 1.4e-06;  
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFSGIWRFLRFAYG 18  
 ||||:|||||:||||  
 Db 1 GIRKFLGAIWRFIRSFYG 18

RESULT 15  
 ADO34276  
 ID ADO34276 standard; peptide; 18 AA.

XX ADO34276;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;  
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;  
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;  
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;  
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1..18 /note= "All Lys residues are DiMethyl-Lysine"

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating  
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis  
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking  
 CC polypeptide. The invention further comprises an isolated nucleic acid  
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,  
 CC a host cell, a recombinant cell or a transgenic, non-human subject  
 CC (including animal or plant) comprising the synthetic apolipoprotein-E  
 CC mimicking polypeptide encoding polynucleotide; a composition comprising  
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and  
 CC an monoclonal antibody that specifically binds to the synthetic  
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E  
 CC mimicking polypeptide has the following activities: antilipaeamic,  
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and  
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is  
 CC useful for reducing serum cholesterol in a subject (including a mammal  
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
 CC chimpanzee or orangutan); for treating coronary artery disease,

CC useful for reducing serum cholesterol in a subject (including a mammal  
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,  
CC chimpanzee or orangutan); for treating coronary artery disease,  
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of  
CC myocardial infarction or stroke; for breaking an embolus in the subject;  
CC and also for treating angina. The synthetic apolipoprotein-E mimicking  
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low  
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or  
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E  
CC mimicking polypeptide of the invention.

XX

SQ Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;  
Best Local Similarity 77.8%; Pred. No. 1.4e-06;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFKAFYG 18  
|||:|||||:|||||  
Db 1 GIKRFLGSIWRFKAFYG 18

Search completed: May 19, 2006, 14:24:30  
Job time : 94.2857 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds  
(without alignments)  
121.233 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRRFIGSIWRFLAFYFG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80: \*  
1: Pirl1: \*  
2: Pirl2: \*  
3: Pirl3: \*  
4: Pirl4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	49.0	627	S76462	hypothetical prote
2	47	48.0	489	B84733	probable cytochrom
3	46	46.9	246	2	MHC HLA-A cell sur
4	46	46.9	273	1	MHC class I histoc
5	46	46.9	365	1	MHC class I histoc
6	46	46.9	365	2	Gene HLA-A-0203 pr
7	46	46.9	365	2	MHC class I histoc
8	46	46.9	365	2	MHC class I histoc
9	46	46.9	365	2	MHC class I histoc
10	46	46.9	365	2	MHC HLA-A2.4a chai
11	46	46.9	365	2	gene HLA-A-0205 pr
12	46	46.9	516	2	hypothetical prote
13	45	45.9	519	1	cytochrome P450 DW
14	45	45.9	719	2	DNA ligase (NAD) (
15	44.5	45.4	760	2	penicillin-binding
16	44	44.9	589	2	poly(3-hydroxybuty
17	44	44.9	806	2	leucyl-tRNA synthet
18	44	44.9	1112	2	probable calcium-a
19	43.5	44.4	790	2	homolog to drosoph
20	43	43.9	178	2	transcription regu
21	42.5	43.4	1025	2	acriflavin resista
22	42	42.9	265	2	rfaP protein - Esc
23	42	42.9	426	2	hypothetical prote
24	42	42.9	803	2	leucyl-tRNA synthet
25	42	42.9	803	2	leucyl-tRNA synthet
26	41.5	42.3	178	2	hypothetical prote
27	41	41.8	131	2	galactosyltransfer
28	41	41.8	207	2	probable pol polyp
29	41	41.8	275	2	

#### ALIGNMENTS

##### RESULT 1

S76462

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S76462

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI000000C103F; EMBL:D90915; GB:AB001339; NID: A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;  
Best Local Similarity 38.9%; Pred. No. 8;  
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLAFYFG 18

Db 597 GLEQLLGKIQWLNQKFG 614

##### RESULT 2

B84733

probable cytochrome P450 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: B84733

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84733

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-489 <STO>

A:Cross-references: UNIPROT:Q9V272; UNIPARC:UPI000000D9B8; GB:AE002093; NID:g3831452; PII: C:Genetics:

A:Gene: At2g32440

A:Map position: 2

C:Superfamily: Synecocystis cytochrome P450 slr0574; cytochrome P450 homology

Query Match 48.0%; Score 47; DB 2; Length 489;

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Best Local Similarity 72.7%; Pred. No. 9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IGSIRFLRAF 16
   ||::|||
Db 54 IGNNWFLRAF 64

RESULT 3
I54412
MHC HLA-A cell surface antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54412
R:Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A:Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A:Reference number: I54412; MUID:84287690; PMID:6332068
A:Accession: I54412
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-246 <RES>
A:Cross-references: UNIPROT:Q29945; UNIPARC:UPI000008A27D; GB:M27537; NID:g187727; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: surface antigen
F:101-166/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 246;
Best Local Similarity 58.3%; Pred. No. 6.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLRAF 17
   |||||::
Db 8 VGSDWFLRGYH 19

RESULT 4
HLHU69
MHC class I histocompatibility antigen HLA-Aw69 alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: B24671
R:Holmes, N.; Parham, P.
EMBO J. 4, 2849-2854, 1985
A:Title: Exon shuffling in vivo can generate novel HLA class I molecules.
A:Reference number: A91021; MUID:86055720; PMID:3877632
A:Accession: B24671
A:Molecule type: DNA
A:Residues: 1-273 <HOL>
A:Cross-references: UNIPROT:P10316; UNIPARC:UPI0000124E4B
C:Genetics:
A:Gene: GDB:HLA-A
A:Cross-references: GDB:119310; OMIM:142800
A:Map position: 6p21.3-6p21.3
A:Introns: 89/3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F:195-260/Domain: immunoglobulin homology <IMM>
F:85/Binding site: carbohydrate (asn) #status predicted

Query Match 46.9%; Score 46; DB 1; Length 273;
Best Local Similarity 59.3%; Pred. No. 7.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLRAF 17
   |||||::
Db 102 VGSDWFLRGYH 113

RESULT 5
HLHUA2
MHC class I histocompatibility antigen HLA-A2 alpha chain precursor [validated] - human
C:Species: Homo sapiens (man)

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C:Date: 28-Feb-1980 #sequence_revision 22-Apr-1995 #text_change 08-Dec-2000
C:Accession: I55948; E35997; A02191; S19020; S77965; S23593; A93834; A93919; S14802; A0201
R:Koller, B.H.; Orr, H.T.
J. Immunol. 134, 2727-2733, 1985
A:Title: Cloning and complete sequence of an HLA-A2 gene: Analysis of two HLA-A alleles
A:Reference number: I55948; MUID:85132727; PMID:2982951
A:Accession: I55948
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-365 <KOL>
A:Cross-references: UNIPARC:UPI0000124E24; GB:K02883; NID:g187605; PIDN:AAA98727.1; PID:
A:Experimental source: lymphoblastoid cell line 721
R:Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A:Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency
A:Reference number: A35997; MUID:90207291; PMID:2320591
A:Accession: E35997
A:Molecule type: mRNA
A:Residues: 1-365 <ENN>
A:Cross-references: UNIPARC:UPI0000124E24; GB:M84379; GB:M32322; NID:g403143; PIDN:AAA59
A:Note: this allele is designated A*0201 (previously HLA-A2.1)
R:Kragel, M.S.
EMBO J. 4, 1205-1210, 1985
A:Title: Unusual RNA splicing generates a secreted form of HLA-A2 in a mutagenized B lymph
A:Reference number: A02191; MUID:85230571; PMID:3874058
A:Accession: A02191
A:Molecule type: mRNA
A:Residues: 39-365 <KRA>
A:Cross-references: UNIPARC:UPI000016AA56; GB:X02457; NID:g32153; PIDN:CAA26297.1; PID:
A:Note: the author translated the codon CAG for residue 96 as His, ACU for residue 97 as
s Thr, and ACU for residue 323 as Ser
R:Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 34, 281-285, 1991
A:Title: Structure of the HLA-A*0204 antigen, found in South American Indians. Spatial cl
A:Reference number: S19020; MUID:92039809; PMID:1937577
A:Accession: S19020
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 9-120, 'M', 122-365 <CAS1>
A:Cross-references: UNIPARC:UPI00001737ED; EMBL:X57954; NID:g32150
A:Note: this allele is designated A*0204
A:Note: the sequence in GenBank entry HSHLAA020, release 106.0, (PID:g32151) differs beca
R:Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Nature 357, 326-329, 1992
A:Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A:Reference number: I37120; MUID:92289555; PMID:1317015
A:Accession: S77965
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-365 <BEL>
A:Cross-references: UNIPARC:UPI0000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PI
A:Experimental source: cell line GRC 138; isolate A*0201
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R:Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 35, 344-346, 1992
A:Title: Structure of the HLA-A*0211 (A2.5) subtype: further evidence for selection-driv
A:Reference number: S23593; MUID:92218010; PMID:1559719
A:Accession: S23593
A:Molecule type: mRNA
A:Residues: 9-96, 'ID', 99-365 <CAS2>
A:Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:g32156; PIDN:CAB56609.1; PID:
A:Note: this allele is designated A*0211 (previously HLA-A2.5)
R:Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
Proc. Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979
A:Title: Comparison of amino acid sequences of two human histocompatibility antigens, HL
A:Reference number: A93834; MUID:80056745; PMID:92029
A:Accession: A93834
A:Molecule type: protein
A:Residues: 25-55, 'Z', 57-60, 'B', 62, 'B', 64-66, 'Z', 68-74, 'X', 76-85, 'RXXX', 90-94, 'AH', 97, 'V'
A:Cross-references: UNIPARC:UPI00001737EE
A:Note: this sequence has been revised in reference A93919
R:Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982

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C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 23-Jul-1999  
 C;Accession: I61902  
 R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Nature 357, 326-329, 1992  
 A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
 A;Reference number: I37120; MUID:92269955; PMID:1317015  
 A;Accession: I61902  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-365 <RES>  
 A;Cross-references: UNIPARC:UPI000016AD39; GB:M84378; NID:G187625; PIDN:AAA59604.1; PID: F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted <IMM>  
 C;Genetics:  
 A;Gene: GDB:HLA-A  
 A;Cross-references: GDB:119310; OMIM:142800  
 A;Map position: 6p21.3-6p21.3  
 A;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplanted  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status experimental  
 F;110/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F;125-188,227-283/Disulfide bonds: #status predicted

Query Match 46.9%; Score 46; DB 1; Length 365;  
 Best Local Similarity 58.3%; Pred. No. 9.8;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLAFY 17  
 :||| ||||| :  
 Db 127 VGSDWRLRGVH 138

RESULT 6  
 I38443  
 gene HLA-A-0203 protein - human  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
 C;Accession: I38443  
 R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P. J. Immunol. 139, 936-941, 1987  
 A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A2  
 A;Reference number: I38441; MUID:87252273; PMID:3496393  
 A;Accession: I38443  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-365 <RES>  
 A;Cross-references: UNIPARC:UPI000016A06E; EMBL:U03863; NID:G432438; PIDN:AAA03604.1; PI  
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 365;  
 Best Local Similarity 58.3%; Pred. No. 9.8;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLAFY 17  
 :||| ||||| :  
 Db 127 VGSDWRLRGVH 138

RESULT 7  
 I61902  
 MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A\*021  
 C;Species: Homo sapiens (man)  
 A;Variety: isolate A\*0212

C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 23-Jul-1999  
 C;Accession: I61902  
 R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Nature 357, 326-329, 1992  
 A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
 A;Reference number: I37120; MUID:92269955; PMID:1317015  
 A;Accession: I61902  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-365 <RES>  
 A;Cross-references: UNIPARC:UPI000016AD39; GB:M84378; NID:G187625; PIDN:AAA59604.1; PID: F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted <IMM>  
 C;Genetics:  
 A;Gene: GDB:HLA-A  
 A;Cross-references: GDB:119310; OMIM:142800  
 A;Map position: 6p21.3-6p21.3  
 A;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C;Keywords: transmembrane protein  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted <IMM>  
 F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 365;  
 Best Local Similarity 58.3%; Pred. No. 9.8;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLAFY 17  
 :||| ||||| :  
 Db 127 VGSDWRLRGVH 138

RESULT 8  
 I37542  
 MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A\*0216) precursor - hun  
 C;Species: Homo sapiens (man)  
 C;Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000  
 C;Accession: I37542; S49582  
 R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J. Immunogenetics 41, 388, 1995  
 A;Title: Identification of a novel HLA-A2 subtype, HLA-A\*0216.  
 A;Reference number: I37542; MUID:95278976; PMID:7759139  
 A;Accession: I37542  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-365 <RES>  
 A;Cross-references: UNIPARC:UPI000016AA63; EMBL:Z46633; NID:G575248; PIDN:CAA86602.1; PI  
 A;Note: submitted to the EMBL Data Library, November 1994  
 C;Genetics:  
 A;Gene: hla-A  
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 365;  
 Best Local Similarity 58.3%; Pred. No. 9.8;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLAFY 17  
 :||| ||||| :  
 Db 127 VGSDWRLRGVH 138

RESULT 9  
 I84448  
 MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A\*021  
 C;Species: Homo sapiens (man)  
 A;Variety: isolate A\*0211  
 C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 23-Jul-1999  
 C;Accession: I84448  
 R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Nature 357, 326-329, 1992  
 A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.  
 A;Reference number: I37120; MUID:92269955; PMID:1317015  
 A;Accession: I84448

A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:g187623; PIDN:AAAS9603.1; PID:  
A;Experimental source: cell line GRC 138; isolate A\*0211  
C;Genetics:  
A;Gene: GDB:HLA-A  
A;Cross-references: GDB:119310; OMIM:142800  
A;Map position: gp21.3-6p21.3  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted  
F;220-285/Domain: immunoglobulin homology <IMM>  
Query Match 46.9%; Score 46; DB 2; Length 365;  
Best Local Similarity 58.3%; Pred. No. 9.8;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 IGSWRFRLAFY 17  
Db 127 VGSDWRFRLRGYH 138  
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RESULT 10  
I61857  
MHC HLA-A2.4a chain - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I61857  
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
J. Immunol. 142, 3937-3950, 1989  
A;Title: Diversity and diversification of HLA-A,B,C alleles.  
A;Reference number: I36956; MUID:89235215; PMID:2715640  
A;Accession: I61857  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016AD48; GB:M24042; NID:g187777; PIDN:  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>  
Query Match 46.9%; Score 46; DB 2; Length 365;  
Best Local Similarity 58.3%; Pred. No. 9.8;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 IGSWRFRLAFY 17  
Db 127 VGSDWRFRLRGYH 138  
::: ||||| :::  
RESULT 11  
I38442  
gene HLA-A-0205 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I38442  
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.  
J. Immunol. 139, 936-941, 1987  
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A2  
A;Reference number: I38441; MUID:87252273; PMID:3496393  
A;Accession: I38442  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-365 <RES>  
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:g432436; PID  
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F;220-285/Domain: immunoglobulin homology <IMM>  
Query Match 46.9%; Score 46; DB 2; Length 365;  
Best Local Similarity 58.3%; Pred. No. 9.8;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGSWRFRLAFY 17  
Db 127 VGSDWRFRLRGYH 138  
::: ||||| :::  
RESULT 12  
T33269  
hypothetical protein C24B9.13 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33269  
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.  
submitted to the EMBL Data Library, May 1998  
A;Description: The sequence of C. elegans cosmid C24B9.  
A;Reference number: Z21310  
A;Accession: T33269  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-516 <MUR>  
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1  
A;Experimental source: strain Bristol N2; clone C24B9  
C;Genetics:  
A;Gene: CESP:C24B9.13  
A;Map position: 5  
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2  
Query Match 46.9%; Score 46; DB 2; Length 516;  
Best Local Similarity 47.1%; Pred. No. 14;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 IREFIGSIWRFLEAFY 18  
Db 252 LKFFITSLWMFMHAFDG 268  
::: ||||| :::  
RESULT 13  
T02263  
cytochrome P450 DWARF3 - maize  
N;Contains: oxidoreductase (EC 1.-.-.-)  
C;Species: Zea mays (maize)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T02263  
R;Winkler, R.G.; Helentjaris, T.  
Plant Cell 7, 1307-1317, 1995  
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberellin  
A;Reference number: Z14648; MUID:96004534; PMID:7549486  
A;Accession: T02263  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-519 <WIN>  
A;Cross-references: UNIPROT:Q43246; UNIPARC:UPI0000126CF8; EMBL:U32579; NID:g987266; PIDN:  
A;Experimental source: strain B73  
C;Genetics:  
A;Gene: dwarf3  
C;Function:  
A;Description: involved in an early step in gibberellin biosynthesis  
A;Pathway: gibberellin biosynthesis  
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology  
C;Keywords: oxidoreductase  
F;325-488/Domain: cytochrome P450 homology <P45>  
Query Match 45.9%; Score 45; DB 1; Length 519;  
Best Local Similarity 63.6%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 IGSWRFRLAF 16  
Db 82 VGGWAFRLRAF 92  
::: ||||| :::  
RESULT 14  
AG3325  
DNA ligase (NAD) (EC 6.5.1.2) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 31-Dec-2004  
C:Accession: AG3325  
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesha  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AG3325  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-719 <KUR>  
A:Cross-references: UNIPROT:Q8YI56; UNIPARC:UPI0000057D37; GB:AE008917; PIDN:AAL51770.1;  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI0589  
A:Map position: I  
C:Superfamily: DNA ligase (NAD), Liga type  
C:Keywords: ligase

Query Match 45.9%; Score 45; DB 2; Length 719;  
Best Local Similarity 58.3%; Pred. No. 27;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRRFIGSIWREL 13  
Db 102 VRDFGVGYREL 113  
:|:|:|:|:|

RESULT 15  
E84953  
penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)  
C:Species: Buchnera sp.  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002  
C:Accession: E84953  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
A:Reference number: AB4930; MUID:20445173; PMID:10953077  
A:Accession: E84953  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-760 <STO>  
A:Cross-references: UNIPARC:UPI000005B4C8; GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: mrcB; BU200  
C:Superfamily: penicillin-binding protein 1B

Query Match 45.4%; Score 44.5; DB 2; Length 760;  
Best Local Similarity 50.0%; Pred. No. 35;  
Matches 9; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 2 IRRFI-GSIWRFLAFYG 18  
Db 32 INRFNGKVNFPPTSIYG 49  
| | | | | : | | | | |

Search completed: May 19, 2006, 14:39:57  
Job time : 15.2857 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model  
Run on: May 19, 2006, 14:13:32 ; Search time 115.429 seconds  
(without alignments)  
144.247 Million cell updates/sec

Title: US-10-712-447-117  
Perfect score: 98  
Sequence: 1 GIRRFIGSIWFLRAFG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	57.1	670	2	Q25271 LEPDE
2	54	55.1	805	2	Q3APY5_CHLCH
3	53	54.1	488	2	Q84ZW1_PEA
4	51	52.0	735	2	Q9F7V7_RHILV
5	50	51.0	361	2	Q2NUB5_SODGL
6	50	51.0	579	1	KKR7_HUMAN
7	50	51.0	579	1	KKR7_PANTR
8	50	51.0	580	1	KKR7_MOUSE
9	50	51.0	580	1	KKR7_RAT
10	49	50.0	278	2	Q7VV93_BORPE
11	49	50.0	278	2	Q7W7P3_BORPA
12	49	50.0	278	2	Q7WL31_BORBR
13	49	50.0	407	2	Q39L57_BURSK
14	49	50.0	408	2	Q456F4_9BURK
15	49	50.0	408	2	Q4LK44_9BURK
16	49	50.0	506	2	Q5VRM7_ORISA
17	48	49.0	188	2	Q2ILN7_9DELT
18	48	49.0	298	2	Q8R587_MOUSE
19	48	49.0	607	2	Q425W5_DESHA
20	48	49.0	627	2	P74489_SYNY3
21	48	49.0	805	2	Q44QD1_CHLLI
22	48	49.0	816	2	Q43K01_CHLORBI
23	47.5	48.5	577	2	Q36XB4_RHOPA
24	47.5	48.5	577	2	Q37C12_RHOPA
25	47	48.0	376	2	Q8KBA7_CHLTE
26	47	48.0	406	2	Q56YS1_ARATH
27	47	48.0	409	2	Q4BFM2_BURVI
28	47	48.0	486	2	Q5U4I4_XENLA
29	47	48.0	487	2	Q32N49_XENLA
30	47	48.0	489	1	KAO2_ARATH
31	47	48.0	490	2	Q84ZW0_PEA

32	47	48.0	597	2	Q5AUS5_EMENI
33	47	48.0	739	2	Q5NPG9_ZYMONA
34	46	46.9	18	2	Q9TNQ7_HUMAN
35	46	46.9	91	2	Q7YNX8_HUMAN
36	46	46.9	91	2	Q7YNY1_HUMAN
37	46	46.9	91	2	Q86IA8_HUMAN
38	46	46.9	91	2	Q8SNB2_HUMAN
39	46	46.9	162	2	Q4QYZ9_HUMAN
40	46	46.9	166	2	P79495_HUMAN
41	46	46.9	169	2	P78376_HUMAN
42	46	46.9	177	2	Q70PC8_HUMAN
43	46	46.9	180	2	Q5DSC6_HUMAN
44	46	46.9	181	2	O19520_HUMAN
45	46	46.9	181	2	O19671_HUMAN

ALIGNMENTS

RESULT 1  
Q25271 LEPDE  
ID Q25271\_LEPDE PRELIMINARY; PRT; 670 AA.  
AC Q25271; 1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE Diapause protein 1 (Fragment).  
GN Name=Dp19;  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;  
OC Chrysomelidae; Chrysomelidae; Chrysomelinae; Doryphorini;  
OC Leptinotarsa.  
OX NCBI\_TaxID=7539;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA de Kort C.A.B., Koopmanschap A.B.;  
RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylin-type storage hexamer of the Colorado potato beetle."  
RL J. Insect Physiol. 40:527-535(1994).

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CC -----  
EMBL; X76080; CAA53691.1; -; mRNA.  
DR HSSP; P04253; 1LL1.  
DR GO; GO:0005344; F:oxygen transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000896; Hemocyanin.  
DR InterPro; IPR005203; hemocyanin C.  
DR InterPro; IPR005204; hemocyanin N.  
DR PANTHER; PTHR11511; Hemocyanin; 1.  
DR Pfam; PF03723; Hemocyanin\_C; 1.  
DR Pfam; PF00372; Hemocyanin\_M; 1.  
DR Pfam; PF03722; Hemocyanin\_N; 1.  
DR PRINTS; PR00187; HAEMOCYANIN.  
DR PROSITE; PS00210; HAEMOCYANIN\_2; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 670 AA; 79825 MW; 8A000BA15B5C8A6 CRC64;

Query Match 57.1%; Score 56; DB 2; Length 670;

Best Local Similarity 50.0%; Pred. No. 4.3;

Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFIGSIWFLRAFG 18

| : | : | : | : | : |

Db 351 RKFYCALMSYLRHFFG 366

RESULT 2

Q3APY5\_CHLCH

ID Q3APY5\_CHLCH PRELIMINARY; PRT; 805 AA.

AC Q3APV5; 22-NOV-2005, integrated into UniProtKB/TrEMBL.  
 DT 21-NOV-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 5.  
 DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).  
 GN OrderedLocusNames=Cag.1688;  
 OS Chlorobium chlorochromatii (strain Cag3).  
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
 OC Chlorobium/Pelodictyon group; Chlorobium.  
 RN NCBI\_TaxID=340177;  
 RX [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RG US DOE Joint Genome Institute;  
 RA Copeland A., Lucas S., Lepidus A., Barry K., Dettler J.C., Glavina T.,  
 RA Hammon N., Israni S., Pfluck S., Bryant D., Schmutz J., Larimer F.,  
 RA Land M., Kyripides N., Ivanova N., Richardson P.,  
 RT "Complete sequence of Chlorobium chlorochromatii Cag3.";  
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: CP000108; AB28940.1. -; Genomic\_DNA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004823; F:leucine-tRNA ligase activity; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR GO: GO:0006429; P:leucyl-tRNA aminocyclization; IEA.  
 KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.  
 SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;  
 QY Query Match 55.1%; Score 54; DB 2; Length 805;  
 Best Local Similarity 61.5%; Pred. No. 11;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GIRRFIGSIWRF 13  
 |||:|:|:|:  
 DB 622 GISRFLGKVRV 634  
 RESULT 3  
 ID Q84ZWL\_PEA PRELIMINARY; PRT; 488 AA.  
 AC Q84ZWL;  
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 21.  
 DE Ent-kaurenoic acid oxidase.  
 GN Name=KA01;  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Shoot;  
 RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;  
 RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;  
 RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";  
 RL Plant Physiol. 131:335-344(2003).  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By  
 similarity).  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -----  
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 CC -----  
 CC EMBL: AF537321; AA023063.1. -; mRNA.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0020037; F:heme binding; IEA.  
 DR GO: GO:0005506; F:iron ion binding; IEA.  
 DR GO: GO:0046872; F:metal ion binding; IEA.  
 DR GO: GO:0004497; F:monooxygenase activity; IEA.

DR GO: GO:0006118; P:electron transport; IEA.  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR InterPro: IPR002401; EP4501.  
 DR PANTHER: PTHR19383; Cytochrome\_P450; 1.  
 DR Pfam: PF00067; P450; 2.  
 DR PRINTS: PR00463; EP4501.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN 1.  
 KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;  
 KW Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;  
 QY Query Match 54.1%; Score 53; DB 2; Length 488;  
 Best Local Similarity 75.0%; Pred. No. 9.5;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 FIGSIWRFRLAP 16  
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 DB 54 FIGMWSFLRAP 65  
 RESULT 4  
 ID Q9F7V7\_RHLV PRELIMINARY; PRT; 735 AA.  
 AC Q9F7V7;  
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 25.  
 DE ABC transporter RzcB.  
 GN Name=rzcB;  
 OS Rhizobium leguminosarum bv. viciae.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=387;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=305;  
 RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;  
 RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;  
 RT "Analysis of the genetic region encoding a novel rhizobiocin from  
 RT Rhizobium leguminosarum bv. viciae strain 305.";  
 RL Can. J. Microbiol. 47:495-502(2001).  
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 CC -----  
 CC EMBL: AF273216; AAG25076.1. -; Genomic\_BNA.  
 DR HSP; P08716; IMTO.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0016887; F:ATPase activity; IEA.  
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.  
 DR GO: GO:0000166; F:nucleotide binding; IEA.  
 DR GO: GO:0008233; F:peptidase activity; IEA.  
 DR GO: GO:0008565; F:protein transporter activity; IEA.  
 DR GO: GO:0015031; P:protein transport; IEA.  
 DR GO: GO:0006508; P:proteolysis; IEA.  
 DR InterPro: IPR003593; AAA\_Atase.  
 DR InterPro: IPR011527; ABC\_TM 1.  
 DR InterPro: IPR001140; ABC\_TM transp.  
 DR InterPro: IPR003439; ABC\_transp.like.  
 DR InterPro: IPR005074; Peptidase\_C39.  
 DR InterPro: IPR010132; Type\_I\_sec\_HlyB.  
 DR PANTHER: PTHR15242:SF74; Type\_I\_sec\_HlyB; 1.  
 DR Pfam: PF00664; ABC membrane; 1.  
 DR Pfam: PF00005; ABC tran; 1.  
 DR Pfam: PF03412; Peptidase\_C39; 1.  
 DR ProDom: PD000006; ABC\_transporter; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR TIGRFAMs: TIGR01846; type\_I\_sec\_HlyB; 1.  
 DR PROSITE: PS50929; ABC\_TM1f; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER 1; 1.  
 DR PROSITE: PS50893; ABC\_TRANSPORTER\_2; 1.

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DR PROSITE; PSS0990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 52.0%; Score 51; DB 2; Length 735;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLRAF 16
    | | | | | | | |
Db 161 GFWFLPAWRYRRAF 176

RESULT 5
Q2NUB5_SODGL PRELIMINARY; PRT; 361 AA.
AC Q2NUB5_
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Putative glycosyltransferase.
GN ORFNAMES=SG0985;
OS Sodalis glossinidius str. 'morsitans'.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=343509;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Morsitans;
RA Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Akao S.;
RT "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156(2006).
CC -----
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CC -----
DR EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
KW Transferase.
SQ SEQUENCE 361 AA; 40247 MW; 1257F70F3C3CA65C CRC64;

Query Match 51.0%; Score 50; DB 2; Length 361;
Best Local Similarity 69.2%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 RFIGSIWRFLRAF 16
    | | | | | | | |
Db 62 RDVGSPWRFLSAF 74

RESULT 6
XKR7_HUMAN STANDARD; PRT; 579 AA.
ID XKR7_HUMAN
AC QSGH72; Q9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
OS Homo sapiens (Human).
GN Name=XKR7; Synonyms=C20orf159, XRG7;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RA LeHvaslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; AY534245; AAT07094.1; -; mRNA.
DR EMBL; AL031658; CAB88102.1; ALT SEQ; Genomic_DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
DR HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF64B9ED53D CRC64;

Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLRAF 17
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Db 190 LGQVRYRLALY 201

RESULT 7
XKR7_PANTR STANDARD; PRT; 579 AA.
ID XKR7_PANTR
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrall B.G., Maskell D.J.;  
RA "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica.";  
RL Nat. Genet. 35:32-40(2003).  
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CC -----  
CC EMBL: BX640430; CAE37766.1; -; Genomic\_DNA.  
DR BL0CVC; BP4R519:BP2471-MONOMER; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004672; F:protein kinase activity; IEA.  
DR GO; GO:0004672; F:protein amino acid phosphorylation; IEA.  
DR GO; GO:0006468; P:protein kinase; I.  
DR InterPro; IPR000719; Prot\_kinase;  
DR ProDom; PD000001; Prot\_kinase;  
DR KW Complete proteome; Hypothetical protein; Kinase; Transferase.  
SQ SEQUENCE 278 AA; 31565 MW; 11DDFD84EPEEF8DF CRC64;  
  
Query Match 50.0%; Score 49; DB 2; Length 278;  
Best Local Similarity 52.9%; Pred. No. 23;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 GIRRFGISWRELRAPY 17  
Db 47 GVRRGISYVLRVLRAPF 63  
  
RESULT 12  
Q7WL31 BORBR  
ID Q7WL31 BORBR PRELIMINARY; PRT; 278 AA.  
AC Q7WL31;  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 21-FEB-2006, entry version 14.  
DE Hypothetical protein.  
OS OrderedLocusNames=BB1918;  
GN Bordetella bronchiseptica  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
OX NCBI\_TaxID=518;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=RB50 / ATCC BAA-588;  
RX MEDLINE=22827954; PubMed=12910271; DOI=i0.1038/ng1227;  
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Baeson N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,  
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrall B.G., Maskell D.J.;  
RA "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica.";  
RL Nat. Genet. 35:32-40(2003).  
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CC -----  
CC EMBL: BX640442; CAE32415.1; -; Genomic\_DNA.  
DR BL0CVC; BBR0518:BB1918-MONOMER; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004672; F:protein kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot\_kinase;  
DR ProDom; PD000001; Prot\_kinase;  
DR KW Complete proteome; Hypothetical protein; Kinase; Transferase.  
SQ SEQUENCE 278 AA; 31507 MW; 6DDDEBFID728D768 CRC64;

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Query Match          50.0%; Score 49; DB 2; Length 278;
Best Local Similarity 52.9%; Pred. No. 23;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFTGSIWRFLRPFY 17
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Db 47 GVRGSIYVLRYPF 63

RESULT 13
Q39L57_BURS3
ID Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
AC Q39L57_BURS3
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocustNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
   / NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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DE Hypothetical protein.
DR EMBL; CP000151; AB06809.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match          50.0%; Score 49; DB 2; Length 407;
Best Local Similarity 41.2%; Pred. No. 35;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFTGSIWRFLRPFY 17
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Db 327 GIRQMLGHVWQWTRSSY 343

RESULT 14
Q456F4_9BURK
ID Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=BcenDRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=AU 1054;
RC US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
   AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

Query Match          50.0%; Score 49; DB 2; Length 408;
Best Local Similarity 41.2%; Pred. No. 35;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFTGSIWRFLRPFY 17
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Db 328 GIRQMLGHVWQWTRSSY 344

RESULT 15
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ID Q4LK44_9BURK PRELIMINARY; PRT; 408 AA.
AC Q4LK44;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_1071;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=HI2424;
RC US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
   HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=HI2424;
RC US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
   HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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DE Hypothetical protein.
DR EMBL; AAHL01000063; EAM16412.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;

Query Match          50.0%; Score 49; DB 2; Length 408;
Best Local Similarity 41.2%; Pred. No. 35;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFTGSIWRFLRPFY 17
   ||| : | : | : | : |

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Db 328 GIRQMLGHVWQWTRSSY 344

Search completed: May 19, 2006, 14:38:13  
Job time : 116.429 secs

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Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFGISWRFLLAFVG 18
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Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFGISWRFLLAFVG 18
   ||::||::||::||::||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
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; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFGISWRFLLAFVG 18
   ||::||::||::||::||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFGV 18
||::|||::|||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 26-NOV-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

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;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFGV 18
||::|||::|||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
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US-09-453-838-242
Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLRAFG 18
   ||:::|||||:|::| |
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7
US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLRAFG 18
   ||:::|||||:|::| |
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
US-09-453-841-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLRAFG 18
   ||:::|||||:|::| |
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9
US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```



STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA: US/09/453,833  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6602854e  
US-09-453-833-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 4.8e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRPFYVG 18  
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 10  
US-09-453-826-242  
Sequence 242, Application US/09453826  
Patent No. 6630450  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,826  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6630450e  
US-09-453-826-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 4.8e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRPFYVG 18  
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 11  
US-09-453-840-242  
Sequence 242, Application US/09453840  
Patent No. 6716816  
GENERAL INFORMATION:  
APPLICANT: Dasseux, Jean-Louis  
APPLICANT: Sekul, Renate  
APPLICANT: Buttner, Klaus  
APPLICANT: Cornut, Isabelle  
APPLICANT: Metz, Gunther  
APPLICANT: Dufourcq, Jean  
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS  
NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,840  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/940,095  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009196-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 242:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6716816e  
US-09-453-840-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 4.8e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFISIWRFLEAFYV 18  
|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFV 18

## RESULT 12

US-09-865-989-242  
; Sequence 242, Application US/09865989  
; Patent No. 6734169  
; GENERAL INFORMATION:  
; APPLICANT: Dasseux, Jean-Louis  
; Sekul, Renate  
; Buttner, Klaus  
; Cornut, Isabelle  
; Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS  
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,989

FILING DATE: 25-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/465,719

FILING DATE: 17-DEC-1999

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0006-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6734169e

SEQUENCE DESCRIPTION: SEQ ID NO: 242:

US-09-865-989-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 4.8e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFISIWRFLEAFYV 18  
|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFV 18

## RESULT 13

US-09-453-834-242  
; Sequence 242, Application US/09453834  
; Patent No. 6753313  
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/453,834

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/940,095

; FILING DATE: 29-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0004-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6753313e

US-09-453-834-242

Query Match 75.5%; Score 74; DB 2; Length 18;  
Best Local Similarity 61.1%; Pred. No. 4.8e-05;  
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFISIWRFLEAFYV 18  
|:::|:::|:::|  
Db 1 GIKKFLGSIWKFIKAFV 18

## RESULT 14

US-10-283-599-242  
; Sequence 242, Application US/10283599  
; Patent No. 6844327  
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: GENE THERAPY APPROACHES TO

; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,599

FILING DATE: 29-OCT-2002

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,136

FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0007-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6844327e

US-10-283-599-242

Query Match

Best Local Similarity 75.5%; Score 74; DB 2; Length 18;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

Sequence 242, Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/465,718

FILING DATE: 17-Dec-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/940,096

FILING DATE: 29-SEP-1997

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6900177e

US-09-465-718-242

Query Match

Best Local Similarity 75.5%; Score 74; DB 2; Length 18;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55

Job time : 25.8571 secs

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OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds  
(without alignments)  
102.575 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRFIGSIWRFLAFYFG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications\_AA\_Main.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pgp.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pgp.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pgp.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pgp.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pgp.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pgp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-117
2	94	95.9	18	4	US-10-712-447-2
3	94	95.9	18	4	US-10-712-447-5
4	94	95.9	18	4	US-10-712-447-8
5	94	95.9	18	4	US-10-712-447-10
6	94	95.9	18	4	US-10-712-447-13
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-127
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	91	92.9	18	4	US-10-712-447-91
13	88	89.8	18	4	US-10-712-447-21
14	88	89.8	18	4	US-10-712-447-53
15	88	89.8	18	4	US-10-712-447-74
16	86	87.8	18	4	US-10-712-447-4
17	86	87.8	18	4	US-10-712-447-113
18	85	86.7	18	4	US-10-712-447-99
19	84	85.7	18	4	US-10-712-447-18
20	84	85.7	18	4	US-10-712-447-112
21	84	85.7	18	4	US-10-712-447-114
22	83	84.7	18	4	US-10-712-447-17
23	83	84.7	18	4	US-10-712-447-121
24	82	83.7	18	4	US-10-712-447-61
25	82	83.7	18	4	US-10-712-447-82
26	81	82.7	18	4	US-10-712-447-16
27	81	82.7	18	4	US-10-712-447-96

Sequence 22, Appl  
Sequence 78, Appl  
Sequence 95, Appl  
Sequence 120, Appl  
Sequence 19, Appl  
Sequence 56, Appl  
Sequence 58, Appl  
Sequence 77, Appl  
Sequence 79, Appl  
Sequence 80, Appl  
Sequence 94, Appl  
Sequence 57, Appl  
Sequence 100, Appl  
Sequence 41, Appl  
Sequence 110, Appl  
Sequence 118, Appl  
Sequence 97, Appl  
Sequence 242, Appl

28 80 81.6 18 4 US-10-712-447-22  
29 80 81.6 18 4 US-10-712-447-78  
30 80 81.6 18 4 US-10-712-447-95  
31 80 81.6 18 4 US-10-712-447-120  
32 78 79.6 18 4 US-10-712-447-19  
33 78 79.6 18 4 US-10-712-447-56  
34 78 79.6 18 4 US-10-712-447-58  
35 78 79.6 18 4 US-10-712-447-77  
36 78 79.6 18 4 US-10-712-447-79  
37 78 79.6 18 4 US-10-712-447-80  
38 78 79.6 18 4 US-10-712-447-94  
39 77 78.6 18 4 US-10-712-447-57  
40 77 78.6 18 4 US-10-712-447-100  
41 76 77.6 18 4 US-10-712-447-41  
42 76 77.6 18 4 US-10-712-447-110  
43 76 77.6 18 4 US-10-712-447-118  
44 75 76.5 18 4 US-10-712-447-97  
45 74 75.5 18 3 US-09-865-989-242

#### ALIGNMENTS

##### RESULT 1

US-10-712-447-117  
; Sequence 117, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GABBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10712.447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 117  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-117

Query Match 100.0%; Score 98; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFIGSIWRFLAFYFG 18  
Db 1 GIRFIGSIWRFLAFYFG 18

##### RESULT 2

US-10-712-447-2  
; Sequence 2, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GABBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT APPLICATION NUMBER: US/10712.447  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13

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; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRRFLGSIWRFLRAFYG 18
|||||:|||||:|||||

RESULT 3
US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRRFLGSIWRFLRAFYG 18
|||||:|||||:|||||

RESULT 4
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRRFLGSIWRFLRAFYG 18
|||||:|||||:|||||

RESULT 5
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRRFLGSIWRFLRAFYG 18
|||||:|||||:|||||

RESULT 6
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFG 18
   |::|::|::|::|::|
Db 1 GIRRFLGSIWRFLRAFG 18

RESULT 7
US-10-712-447-115
; Sequence 115, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-115

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFG 18
   |::|::|::|::|::|
Db 1 GLRRFIGSIWRFLRAFG 18

RESULT 8
US-10-712-447-116
; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 116
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFG 18
   |::|::|::|::|::|
Db 1 GLRRFIGSIWRFLRAFG 18

RESULT 9
US-10-712-447-127
; Sequence 127, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 127
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-127

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFG 18
   |::|::|::|::|::|
Db 1 GLRRFIGSIWRFLRAFG 18

RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-129
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Query Match 95.9%; Score 94; DB 4; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.7e-07;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGIWRFLRAFG 18  
| | | | | : | | | | | : | | | | |  
Db 1 GIRFLGSLWRFLRAFG 18

RESULT 11  
US-10-712-447-131  
; Sequence 131, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 131  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-131

Query Match 95.9%; Score 94; DB 4; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.7e-07;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGIWRFLRAFG 18  
| | | | | : | | | | | : | | | | |  
Db 1 GLRFLGSIWRFLRAFG 18

RESULT 12  
US-10-712-447-91  
; Sequence 91, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 91  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-91

Query Match 92.9%; Score 91; DB 4; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1e-06;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGIWRFLRAFG 18  
| | | | | : | | | | | : | | | | |  
Db 1 GIRKFLGSIWRFLRAFG 18

RESULT 13  
US-10-712-447-21  
; Sequence 21, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-712-447-21

Query Match 89.8%; Score 88; DB 4; Length 18;  
Best Local Similarity 77.8%; Pred. No. 3e-06;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGIWRFLRAFG 18  
| | | | | : | | | | | : | | | | |  
Db 1 GIRRFLGAIWRFLRAFG 18

RESULT 14  
US-10-712-447-53  
; Sequence 53, Application US/10712447  
; Publication No. US20040186057A1  
; GENERAL INFORMATION:  
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.  
; APPLICANT: GARBER, DAVID W.  
; APPLICANT: DATTA, GEETA  
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING  
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE  
; FILE REFERENCE: 112739-123US  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/425,821  
; PRIOR FILING DATE: 2002-11-13  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 53  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (3)  
; OTHER INFORMATION: (DiMe)Lys  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (14)



Tue May 23 08:37:59 2006

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; OTHER INFORMATION: (Dime)Lys
US-10-712-447-53
Query Match      89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRRFIGSIWRFLRAFYG 18
      |||:|||||:|||||
Db      1 GKRFLGSIWRFLRAFYG 18

RESULT 15
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match      89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRRFIGSIWRFLRAFYG 18
      |||:|||||:|||||
Db      1 GKRFLGSIWRFLRAFYG 18
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Search completed: May 19, 2006, 15:27:57  
Job time : 82.2857 secs

***This Page Blank (uspto)***

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OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 seconds  
(without alignments)  
17.943 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRRFIGSIWFLRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US09 NEW PUB.psp:\*\*
- 2: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US06 NEW PUB.psp:\*\*
- 3: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US07 NEW PUB.psp:\*\*
- 4: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US08 NEW PUB.psp:\*\*
- 5: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/PCT\_NEW PUB.psp:\*\*
- 6: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US10 NEW PUB.psp:\*\*
- 7: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US11 NEW PUB.psp:\*\*
- 8: /EMC Celleria\_SIDS3/ptodata/2/pubpaa/US60\_NEW PUB.psp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37.5	38.3	441	6	US-10-511-937-2947	Sequence 2947, Ap
2	36	36.7	74	1	US-09-949-925-111	Sequence 111, App
3	35	35.7	313	7	US-11-242-505A-48	Sequence 48, Appl
4	35	35.7	342	7	US-11-204-427-7	Sequence 7, Appli
5	35	35.7	403	7	US-11-242-505A-18	Sequence 18, Appl
6	35	35.7	667	7	US-11-311-555-16	Sequence 16, Appl
7	35	35.7	667	7	US-11-311-561-16	Sequence 16, Appl
8	35	35.7	764	7	US-11-223-738-6	Sequence 6, Appli
9	34	34.7	447	6	US-10-975-692-2	Sequence 2, Appli
10	34	34.7	599	7	US-11-302-678-5	Sequence 5, Appli
11	34	34.7	627	7	US-11-249-111-88	Sequence 88, Appl
12	33	33.7	643	6	US-10-504-120-19	Sequence 19, Appl
13	33	33.7	651	6	US-10-511-937-2401	Sequence 2401, Ap
14	33	33.7	714	6	US-10-868-498-2	Sequence 2, Appli
15	33	33.7	749	6	US-10-505-928-443	Sequence 443, App
16	33	33.7	919	7	US-11-302-678-62	Sequence 62, Appl
17	32.5	33.2	60	1	US-09-949-925-142	Sequence 142, App
18	32.5	33.2	4590	6	US-10-505-928-569	Sequence 569, App
19	32	32.7	364	7	US-10-511-937-2540	Sequence 2540, Ap
20	32	32.7	364	7	US-11-113-081A-6	Sequence 6, Appli
21	32	32.7	388	6	US-10-196-749-336	Sequence 336, App
22	32	32.7	388	7	US-11-024-544A-169	Sequence 169, App
23	32	32.7	388	7	US-11-190-750-137	Sequence 137, App
24	32	32.7	388	7	US-11-204-427-1	Sequence 1, Appli
25	32	32.7	393	7	US-11-304-129-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-10-511-937-2947  
; Sequence 2947, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fy, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, Macdonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2947  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2947

Query Match 38.3%; Score 37.5; DB 6; Length 441;

Best Local Similarity 33.3%; Pred. No. 13;

Matches 7; Conservative 5; Mismatches 6; Indels 3; Gaps 1;

Qy 1 GIRRFIGSIW---RFLRAFYG 18

Db 106 GLSKFLGTHLMGNILRLFLG 126

RESULT 2

US-09-949-925-111  
; Sequence 111, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins

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; FILE REFERENCE: PZ023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111
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Query Match          36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY      2 IRRFIGSIWRF 12
      :|:|:|:|:|
Db      59 LREVGKIWRF 69

RESULT 3
US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10NM1M
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-48
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Query Match          35.7%; Score 35; DB 7; Length 313;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 WRFLRAFY 17
      :|:|:|:|:|
Db      199 WSFLDAFY 206

RESULT 4
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7
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Query Match          35.7%; Score 35; DB 7; Length 342;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      8 SIWRFLRAFY 17
      :|:|:|:|:|
Db      84 AIWRQLRDY 93

RESULT 5
US-11-242-505A-18
; Sequence 18, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10NM1M
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-18

Query Match          35.7%; Score 35; DB 7; Length 403;
Best Local Similarity 44.4%; Pred. No. 32;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2 IRRFIGSIW 10
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Db 155 VRRVLGAVW 163  
|||:|:|

## RESULT 6

US-11-311-555-16  
; Sequence 16, Application US/11311555  
; Publication No. US20060088916A1

## GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Hanzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tumas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1 (US)

; CURRENT APPLICATION NUMBER: US/11/311,555

; CURRENT FILING DATE: 2005-12-20

; PRIOR APPLICATION NUMBER: US/09/747,259

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US 60/175,481

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US00/04341

; PRIOR FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/191,007

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/07532

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/15264

; PRIOR FILING DATE: 2000-06-02

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 39

; SEQ ID NO 16

; LENGTH: 667

; TYPE: PRT

; ORGANISM: Homo Sapien

US-11-311-555-16

## Query Match

Best Local Similarity 35.7%; Score 35; DB 7; Length 667;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 RRFISITWRFELAFYG 18

|||:|:|

Db 502 RRLVGALAEELRAALG 517

## RESULT 7

US-11-311-561-16

; Sequence 16, Application US/11311561

; Publication No. US20060088917A1

## GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Hanzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tumas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1 (US)

; CURRENT APPLICATION NUMBER: US/11/311,561

; CURRENT FILING DATE: 2005-12-20

; PRIOR APPLICATION NUMBER: US/09/747,259

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US 60/175,481

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US00/04341

; PRIOR FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 60/191,007

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/07532

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: PCT/US00/15264

; PRIOR FILING DATE: 2000-06-02

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 39

; SEQ ID NO 16

; LENGTH: 667

; TYPE: PRT

; ORGANISM: Homo Sapien

US-11-311-561-16

## Query Match

Best Local Similarity 35.7%; Score 35; DB 7; Length 667;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 RRFISITWRFELAFYG 18

|||:|:|

Db 502 RRLVGALAEELRAALG 517

## RESULT 8

US-11-223-738-6

; Sequence 6, Application US/11223738

; Publication No. US20060099682A1

## GENERAL INFORMATION:

; APPLICANT: DELANY, Samantha

; APPLICANT: SANSEAU, Philippe

; APPLICANT: TATE, Simon Nicholas

; TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES

; FILE REFERENCE: PG3606D1

; CURRENT APPLICATION NUMBER: US/11/223,738

; CURRENT FILING DATE: 2005-09-09

; PRIOR APPLICATION NUMBER: 09/857,123

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: PCT/EP99/09284

; PRIOR FILING DATE: 1999-11-30

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; PRIOR APPLICATION NUMBER: GB98263593
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 6
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-223-738-6

Query Match          35.7%; Score 35; DB 7; Length 764;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 GTRFSGIWRFLR 14
      |||:|:|
Db      443 GYLLVQLMYFWR 456

RESULT 9
US-10-975-692-2
; Sequence 2, Application US/10975692
; Publication No. US20060090221A1
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browne, John A
; APPLICANT: Wallis, James G
; APPLICANT: Watts, Jennifer L.
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 4630-58963-02
; CURRENT APPLICATION NUMBER: US/10/975,692
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 09/857,583
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-975-692-2

Query Match          34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      2 IRRFSGIWRFLRAF 17
      |||:|:|
Db      130 IRKILETIFLAF 145

RESULT 10
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: WPI02-012PIRM.OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511

; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-5

Query Match          34.7%; Score 34; DB 7; Length 599;
Best Local Similarity 57.1%; Pred. No. 76;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      6 IGSIRWF 12
      |:|:|
Db      64 LGNWRWF 70

RESULT 11
US-11-249-111-88
; Sequence 88, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; TITLE OF INVENTION: and methods for their use.
; FILE REFERENCE: 13353.1048ulc2
; CURRENT APPLICATION NUMBER: US/11/249,111
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-11-249-111-88

Query Match          34.7%; Score 34; DB 7; Length 627;
Best Local Similarity 55.6%; Pred. No. 80;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 FIGSIWRFL 13
      |:|:|
Db      194 FVGTIWMWL 202

RESULT 12
US-10-504-120-19
; Sequence 19, Application US/10504120
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; Publication No. US20060088829A1
; GENERAL INFORMATION:
; APPLICANT: Exelixis, Inc.
; TITLE OF INVENTION: MINRS AS MODIFIERS OF INSULIN RECEPTOR SIGNALING AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: EX03-003C-PC
; CURRENT APPLICATION NUMBER: US/10/504,120
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: 60/354,824
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/358,217
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,189
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,126
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,995
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/358,756
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/358,765
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,531
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/360,222
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/360,224
; PRIOR FILING DATE: 2002-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-504-120-19

Query Match      33.7%; Score 33; DB 6; Length 643;
Best Local Similarity 38.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      4 RFIGSIWFLRAF 16
Db      482 QFIDCVQMTQF 494

RESULT 13
US-10-511-937-2401
; Sequence 2401, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2401
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; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2401

Query Match      33.7%; Score 33; DB 6; Length 651;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IRRFIGSIW 10
Db      92 LRHFVGWVW 100

RESULT 14
US-10-868-498-2
; Sequence 2, Application US/10868498
; Publication No. US20060099600A1
; GENERAL INFORMATION:
; APPLICANT: MCINTIRE, STEVEN
; TITLE OF INVENTION: A NOVEL ACETYLCHOLINE TRANSPORTER
; FILE REFERENCE: 316T-002510US
; CURRENT APPLICATION NUMBER: US/10/868,498
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/480,508
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-868-498-2

Query Match      33.7%; Score 33; DB 6; Length 714;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GIRRFIGSIWRF 12
Db      79 GFTAGVGSFWKF 90

RESULT 15
US-10-505-928-443
; Sequence 443, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 443
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-443

Query Match      33.7%; Score 33; DB 6; Length 749;
Best Local Similarity 30.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy      2 IRRFIGSIWR 11
Db      272 VKRYVESLWK 281

Search completed: May 19, 2006, 15:28:17
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Job time : 2.14286 secs

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